

Schreiber, David

From: Swope, Sheridan
 Sent: Saturday, December 04, 2004 5:25 PM
 To: Schreiber, David
 Subject: FW: 09/940,235

Scan this page

David Dearest,

Would you do the following alignments for me?

From 09/940,235:

Align SID 4, residues 1-106 with each of the sequences below:

Align SID 4, residues 150-259 with each of the sequences below:

THANK YOU VERY MUCH!!

Pending Data Base

✓ PCT/US93/09502: SID 1
 ✓ US08/128,299: SID 1

A Geneseq Data Base

✓ AAR10194
 ✓ AAR63120
 ✓ AAY24794
 ✓ AAW94664
 ✓ AAY01556
 ✓ AAY24797

UniProt_02 Data Base

✓ STRP_STREQ

Issued Patents Data Base

✓ US 09/211,542: SID 6 6 2 10 66 7

US 07/549,049 (US 5,240,845) SID 1 & SID 2 & SID 3 ←

✓ US 08/560,098: SID 52

✓ US 09/211,542: SID 2 & SID 5 → NA

✓ US 08/568,393B: SID 1

GenEmbl Data Base

✓ E03308
 ✓ AR143998
 ✓ STRSKC
 ✓ SEDEXB
 ✓ I05204

N GeneSeq Data Base

✓ AAX80492
 ✓ AAX16632
 ✓ AAX80497

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2004, 15:00:52 ; Search time 2 Seconds
(without alignments)
2.533 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 600
Sequence: 1 QAQMVPQSPVAVSQSKPG.....SMWDTCTIGAGRGISCTI 106

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 10 seqs, 23900 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 20 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=soft -O=Pending Patents AA.Main:US-09-940-235-4
-DB=* -SUFFIX=pto -OUT=align4_1_106_seq -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=106 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=20
-DOALIGN=200 -THR SCORE=ptc -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPV=6
-NO_XLPXY -NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: /staff_overflow/sdavid-tmp/dec04/swope235/seq/ar143998.gb_pat:*
2: /staff_overflow/sdavid-tmp/dec04/swope235/seq/e03308.gb_pat:*
3: /staff_overflow/sdavid-tmp/dec04/swope235/seq/i05204.gb_pat:*
4: /staff_overflow/sdavid-tmp/dec04/swope235/seq/seqdxb.gb_pat:*
5: /staff_overflow/sdavid-tmp/dec04/swope235/seq/seqdxb.gb_pat:*
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10: /staff_overflow/sdavid-tmp/dec04/swope235/seq/seqdxb.gb_pat:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	7.5	1262	E03308	ACCESSION:E03308
2	44	7.3	2568	STRSKC	ACCESSION:K02986
3	44	7.3	8931	SEDEXB	ACCESSION:X72832
C 4	43	7.2	1262	E03308	ACCESSION:E03308
5	38	6.3	2385	1	AR143998
C 6	38	6.3	2385	1	AR143998
7	38	6.3	2385	8	AAx80497
C 8	38	6.3	2385	8	AAx80497
C 9	38	6.3	8931	4	SEDEXB
10	33.5	5.6	1242	6	AAx16632
11	33.5	5.6	1242	7	AAx80492

12	33.5	5.6	1242	9	us-09-211-542a-5
13	33.5	5.6	1242	10	us-08-568-393b-1
14	33.5	5.6	1401	3	I05204
C 15	28.5	4.8	1242	6	AAx16632
16	28.5	4.8	1242	7	AAx80492
C 17	28.5	4.8	1242	9	us-09-211-542a-5
18	28.5	4.8	1242	10	us-08-568-393b-1
C 19	28.5	4.8	1401	3	I05204
C 20	28.5	4.8	2568	5	STRSKC

ACCESSION:I05204
Streptococcus equi
Streptococcus equi
ACCESSION:I05204
ACCESSION:K02986

ALIGNMENTS

RESULT 1	E03308	LOCUS	E03308	DNA encoding recombinant streptokinase.	1262 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	E03308	ACCESSION	E03308	VERSION	E03308.1	GI:2171525		
KEYWORDS	JP 1992011892-A/1.	SOURCE	synthetic construct	ORGANISM	artificial sequences.			
REFERENCE	1	(bases 1 to 1262)						
AUTHORS	Fujii,S., Katano,T., Majima,E., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.							
TITLE	PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION							
JOURNAL	Patent: JP 1992011892-A 1 16-JAN-1992;							
COMMENT	OTSUKA PHARMACEUTICAL CO. LTD. Artificial gene							
	PN JP 1992011892-A/1							
	PD 16-JAN-1992							
	PF 06-JUL-1990 JP 1990179851							
	PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR 11-APR-1990 JP 90P 96830							
	PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI ONO KENJI,							
	PI SAKATA YASUO, UENOYAMA TSUTOMU							
	PC C12N15/58,C12N1/21,C12N9/70, (C12N1/21,C12R1:19), (C12N9/70, PC C12R1:19);							
	CC strandedness: Double;							
	CC topology: Linear;							
	CC hypothetical: No;							
	CC anti-sense: No;							
	CC *source: clone=PSKX;							
	PH Key							
	FT 5'UTR							
	FT CDS							
	FT							
	mat_peptide							
	3'UTR							
FEATURES	source							
	1..1262							
	/product='recombinant streptokinase' FT							
	/product='recombinant streptokinase' FT							
	1257..1263							
	Location/Qualifiers							
	/organism='synthetic construct'							
	/mol_type='genomic DNA'							
	/db_xref='taxon:32630'							
Alignment Scores:								
Pred. No.:	0.651							
Score:	45.00							
Percent Similarity:	42.86%							
Best Local Similarity:	28.57%							
Query Match:	7.50%							
DB:	2							
US-09-940-235-4 (1-259) x E03308 (1-1262)								
Oy 6 ValGlnPro-----GlnSerProValAlaValSerGlnSerLysProGlyCysTyrAsp 23								

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Db      |||:::||||| ||||| ||||| ||| |||||:::
992 GTACGACCGCGTGACAAAGCTAAACTGCTGTACAACAA-----CCTGGATGCTTT--- 1042

Qy      24 AsnGlyLysHisTyrGlnIleAsnGlnTrp-----GluArg-ThrTyrLeuGlyAs 41

Db      1043 -----CGGTATCATCGAGTACACCTGCTGCTAAAGTAGAAGACAAACCATGACGACAC 1096

Qy      41 nValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProG1 61
      |||:::||||| ||||| ||||| ||| |||||
Db      1097 CAACCGTATCATCACCGTATACATGCGCAACGT-----CGGGA 1135

Qy      61 ualaGluGluThrCysPhe-----AspLysTyrThr 71
      |||:::||||| ||||| ||||| ||| |||||
Db      1136 AGGTGAATAATGCATCTTACCATCTGCGATATGACAAAGACCGTTACACC 1184

RESULT 2
STRSKC      STRSKC      2568 bp      DNA      linear      BCT 26-APR-1993
LOCUS      Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
DEFINITION      K02986
ACCESSION      K02986.1 GI:153808
VERSION      Streptokinase.
KEYWORDS      Streptococcus dysgalactiae subsp. equisimilis
SOURCE      Streptococcus dysgalactiae subsp. equisimilis
ORGANISM      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                Streptococcus.
REFERENCE      1 (bases 1 to 2568)
AUTHORS      Malke,H., Roe,B. and Ferretti,J.J.
TITLE      Nucleotide sequence of the streptokinase gene from Streptococcus
JOURNAL      equisimilis H46A
MEDLINE      Gene 34 (2-3), 357-362 (1985)
PUBMED      85232082
COMMENT      Original source text: S.equisimilis (strain H46A) DNA, clone pMF5.
                Draft entry and hard copy of sequence for [1] kindly provided by
                J.J.Ferretti, 03-SEP-1985.
                The -35 and -10 regions are located at positions 760-765 and
                781-786 respectively and an SD sequence at 808-813. Downstream
                from the coding region inverted repeats (positions 2176-2190 and
                2203-2217) are thought to function as transcription terminators.
                The nucleotide sequence of skc does not support the hypothesis that
                the gene has evolved by duplication and fusion, as suggested by
                internal two-fold AA homologies of its product.
FEATURES
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        819..2141
        /note="prestreptokinase"
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        /protein_id="AAA26974.1"
        /db_xref="GI:153808"
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                FLLSGVRVRYPKEPFIQNAKSDVDEYVQFTPLNPDQDDFRPGLKDTLLKTLAIGD
                TITSBLLAQOASILKNHPGVTIYERDSSIYTHNDIIFRTILPMDQFTYRVKREQ
                AVRINKSKGLNEINTDLISEKYVYLKKGKPYDPDFDRSHLKLFTIKYVDVDTNELL
                KSEQLLTASERNLDLYDPRKAKLLYNLDAFGIMDYTLTGKVEDHDDTNRILT
                VMGKRKPEGENASYHLAYDKDRTYEEREVYLRITGTPIDPNPNDK"
        819..896
        /note="streptokinase signal peptide"
        897..2138
        /product="streptokinase"

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        2.05      Length:      2568
        44.00     Matches:      10
    mat_peptide
        42.86%    Conservative: 8

Alignment Scores:
Pred. No.:      44.00
Score:          42.86%
Percent Similarity:
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Best Local Similarity: 23.81%      Mismatches: 14
Query Match:          7.33%      Indels: 10
DB:                   5          Gaps: 1

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy      2 AlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGlyCys 21
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Db      319 GCAAGACCTCATATTGACCAACCCCACTCAAGTAATAAGCGCTCTT----- 366

Qy      22 TyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThrTyrLeuGlyAsn 41
      |||:::||||| ||||| ||||| ||| |||||
Db      367 -----TTTCGATAAACATGATTTGGGAAATGACATATATTGGTCCC 408

Qy      42 ValLeu 43
      |||:::|||||
Db      409 CTTCCTT 414

RESULT 3
STRSKC      STRSKC      8931 bp      DNA      linear      BCT 17-FEB-1997
LOCUS      S.equisimilis dextb, abc, lrp, skc, rel genes and ORF1.
DEFINITION      X72832
ACCESSION      X72832.1 GI:407876
VERSION      1.6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel
KEYWORDS      gene; skc gene; streptokinase; stringent response-like protein.
SOURCE      Streptococcus dysgalactiae subsp. equisimilis
ORGANISM      Streptococcus dysgalactiae subsp. equisimilis
                Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                Streptococcus.
REFERENCE      1 (bases 3621 to 6190)
AUTHORS      Malke,H., Roe,B. and Ferretti,J.J.
TITLE      Nucleotide sequence of the streptokinase gene from Streptococcus
JOURNAL      equisimilis H46A
MEDLINE      Gene 34 (2-3), 357-362 (1985)
PUBMED      2989113
COMMENT      2 (bases 1 to 4188; 5790 to 8931)
                Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
                Genetic organization of the streptokinase region of the
                Streptococcus equisimilis H46A chromosome
                Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
FEATURES
    JOURNAL      94049672
    MEDLINE      8232196
    PUBMED      8232196
    REFERENCE      3 (bases 1 to 8931)
    AUTHORS      Malke,H.
    TITLE      Direct Submission
    JOURNAL      Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
                Jena University, Winzerlaer Str 10, 07708 Jena, FRG
    COMMENT      Related sequences: K02986, M19346, X13399 & X13400.
    FEATURES
        Location/Qualifiers
            1..8931
            /organism="Streptococcus dysgalactiae subsp. equisimilis"
            /mol_type="genomic DNA"
            /strain="H46A"
            /isolate="human group C strain"
            /sub_species="equisimilis"
            /db_xref="taxon:119602"
            /chromosome="streptokinase region"
            /clone_lib="E.coli plasmid library containing subfragments
                of the submitted seq:pSHD14/16, pSPV19, pSH2, pMF1,
                pCPW73, pRH10, pWX4"
            complement(89..1761)
            /gene="dextb"
            complement(89..115)
            /gene="dextb"
            /note="hairpin loop"
            complement(136..1749)
            /gene="dextb"
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            /codon_start=1
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/product="glucan 1,6-alpha-glucosidase"
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/db_xref="GOA:Q59905"
/db_xref="Swiss-Prot:Q59905"
/translation="MQKQWHRATIQIYIPRSFKDTSGNGIGDLKGITSQLDYLOKLG
ITAIWLSPVYQSPMDNGSPDYIYWRDEPNMLSIPIGSAWELDEASGGYIHLHPSK
HTSDHAWVEAREBNPNDYIYWRDEPNMLSIPIGSAWELDEASGGYIHLHPSK
KOPDLNENAHVRQKIYDMNFIKAGIGGFRMDVLDLGIKIPDSITGNGPRLHPSK
KEMNQATFNGHVTMTVGETWGTGATPEIARQYSRPENKELSMVFQFEHVGLQHKENAPKW
DYAELDLVPAKATYIISKWOTELKLGWNSLFWNNHDLPRVLSIWGNDSTYRKSAKA
LAILLHMGRTYIYVGEIGICWNTVPKDLTEVDVDJESLNYAKEAMENGVPAARVNWS
IRKVRGNARTPMQSKDTHAGFSEAQETWLPVNPYQEIINVADALANQDSIFYTYQQ
LIALRKDDMLVEADYHLLPTADKVFAYQRQGEETVIYVNVSDQEQVPAKDLAAGE
VITITVDVKVLETKHLPQWDAFCVKLSV"
RBS
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complement(1757..1761)
gene
complement(1780..3051)
/gene="abc"
terminator
complement(1780..1810)
/gene="abc"
/note="hairpin loop"
misc_feature
complement(2482..2499)
/gene="abc"
/note="Walker motif B"
CDS
complement(2633..2965)
/gene="abc"
/codon_start=1
/transl_table=11
/product="ABC transporter"
/protein_id="CAA51349.1"
/db_xref="GI:600072"
/db_xref="GOA:Q54086"
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/translation="WVELNLNHIYKYPNTHYAVEDFDLDIKDKSEFIYVFGSGCGK
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complement(2644)
/gene="abc"
misc_feature
/note="(x1) frame shift mutation in H46A"
complement(2828..2854)
/gene="abc"
RBS
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/gene="abc"
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terminator
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CDS
complement(3262..4110)
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/db_xref="GOA:Q54087"
/db_xref="Swiss-Prot:Q54087"
/translation="MELKDYFPEMQVGHPLGDKWVSVKEGDYVHPKSCLSSEKER
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QVAGLEVILPISTTQAFLCQKATSIKVLRSLEGLLPTLESDFGLMTFVGNAMYQ
VAAGTLRECFEECQLLTAYLKQKSGGKLLTFAEVMWLSILSHQSPALTRQPHQLYN
POSDNADVVHAWSEHGNDLVQTAQLRYIHRNSIQYKLDKPAQQSGLHLKQLDLDLAFAY
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4392..5837
/gene="skc"
misc_feature
4392..4393
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4395..4400
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4401..4406
/gene="skc"
-10_signal
4428..4431
/note="alternative"
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/gene="skc"
CDS
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/transl_table=11
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/db_xref="GI:407879"
/db_xref="GOA:P00779"
/db_xref="Swiss-Prot:P00779"
/transl_table=11
/product="unlabeled protein product; ORF1"
complement(5859..6302)
/note="unlabeled protein product; ORF1"
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/db_xref="GOA:Q54088"
/db_xref="Swiss-Prot:Q54088"
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/product="stringent response-like protein"
/protein_id="CAA51353.1"
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/db_xref="GOA:Q54089"

Alignment Scores:

Pred. No.: 8.55 Length: 8931
 Score: 44.00 Matches: 10
 Percent Similarity: 42.86% Conservative: 8
 Best Local Similarity: 23.81% Mismatches: 14
 Query Match: 7.33% Indels: 10
 DB: 4 Gaps: 1

US-09-940-235-4 (1-259) x SEDEXB (1-8931)

Qy 2 AlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGlyCys 21
 Db 3939 GCAAGACCTCATATTGACCAACCCACCTCAAGTAATAAGCGCTCTT----- 3986
 Qy 22 TyrAspAsnGlyLysHisThrGlnIleAsnGlnTrpGluArgThrTyrLeuGlyAsn 41
 Db 3987 -----TTTCGATAAACAATGATTGGGAAAATGCACATATTGGTCCC 4028
 Qy 42 ValLeu 43
 Db 4029 CTCTCT 4034

RESULT 4

E03308/c LOCUS E03308 1262 bp DNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding recombinant streptokinase.

E03308

E03308.1 GI:2171525

JP 1992011892-A/1.

synthetic construct

synthetic construct

artificial sequences.

1 (bases 1 to 1262)

Fuji, S., Katano, T., Majima, E., Ogino, K., Ono, K., Sakata, Y. and

Uenoyama, T.

PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING

PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND

PRODUCTION

Patent: JP 1992011892-A 1 16-JAN-1992;

OTSUKA PHARMACEUTICAL FACTORY INC

OS Artificial gene

PN JP 1992011892-A/1

PD 16-JAN-1992

PF 06-JUL-1990 JP 1990179851

PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR

PI 11-APR-1990 JP 90P 96830

PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI

ONO KENJI,

PI SAKATA YASUYO, UENOYAMA TSUTOMU

PC C12N15/58, C12N1/21, C12N9/70, (C12N1/21, C12R1:19), (C12N9/70, PC

C12R1:19);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC *source: clone=PSKX;

FH Key Location/Qualifiers

FT 5'UTR 1..11

FT CDS 12..1256

FT /product='recombinant streptokinase' FT

mat_peptide 12..1253

FT /product='recombinant streptokinase' FT

FT 3'UTR 1257..1263.

Location/Qualifiers

1..1262

/organism='synthetic construct'

/mol_type='genomic DNA'

/db_xref='taxon:32630'

FEATURES

source

Alignment Scores:

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 Score: 43.00 Matches: 12
 Percent Similarity: 40.30% Conservative: 15
 Best Local Similarity: 17.91% Mismatches: 26
 Query Match: 7.17% Indels: 14
 DB: 2 Gaps: 1

US-09-940-235-4 (1-259) x E03308 (1-1262)

Qy 36 ArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsn 55
 Db 293 AGAATGACCTTACCGATCAGCTGTTCTCGATTGCTTT----- 255

Qy 56 CysGluSerLysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyr 75
 Db 254 -----CAGCAGATCGCTTCTCGATTATGACATAGCGCC 216

Qy 76 ArgValGlyAspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIle 95
 Db 215 AGAGTCAGTAGCGAACGGTTTAGATTTCGGGGACAGCCCTGTTCGGTTTACCACCATG 156

Qy 96 GlyAlaGlyArgGlyArgIle 102
 Db 155 GCGCGGACGAGAGTCAGGTC 135

RESULT 5

AR143998 LOCUS AR143998 2385 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 1 from patent US 6210667.

AR143998

AR143998.1 GI:15105865

Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2385)

AUTHORS Reed, G.L.

TITLE Bacterial fibrin-dependent plasminogen activator

JOURNAL Patent: US 6210667-A 1 03-APR-2001;

FEATURES Location/Qualifiers

1..2385

/organism='unknown'

/mol_type='unassigned DNA'

Alignment Scores:

Pred. No.: 7.15 Length: 2385
 Score: 38.00 Matches: 15
 Percent Similarity: 33.90% Conservative: 5
 Best Local Similarity: 25.42% Mismatches: 35
 Query Match: 6.33% Indels: 4
 DB: 1 Gaps: 1

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 14 ValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGln 33
 Db 933 GTTGGCGAAGATCCACGATTGCCGCACATCGAAGAACGCCAGAAAGGTGAATCAT 992

Qy 34 TrpGluArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGly----- 50
 Db 993 GCCGAACATCCCGCAGATGCCGCTTTCTGTATCGCGTACTCGCGTGATCAACGC 1052

Qy 51 ---SerArgGlyPheAsnCysGluSerLysProGluAlaGluThrCysPheAsp 68
 Db 1053 CGCAGCGGTGTCGACACTGTCGATGAAGCCCTGAAAGACGCGCAGAGCTAATTCGAG 1109

RESULT 6

AR143998/c LOCUS AR143998 2385 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 1 from patent US 6210667.

AR143998

AR143998.1 GI:15105865

Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2385)

AUTHORS Reed, G.L.

TITLE Bacterial fibrin-dependent plasminogen activator

JOURNAL Patent: US 6210667-A 1 03-APR-2001;

FEATURES Location/Qualifiers

1..2385

/organism='unknown'

/mol_type='unassigned DNA'

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2385)

AUTHORS Reed,G.L.

TITLE Bacterial fibrin-dependent plasminogen activator

JOURNAL Patent: US 6210667-A 1 03-APR-2001;

FEATURES Location/Qualifiers

source 1..2385

/organism="unknown"

/mol_type="unassigned DNA"

Alignment Scores:

Pred. No.: 7.15 Length: 2385
Score: 38.00 Matches: 11
Percent Similarity: 38.89% Conservative: 3
Best Local Similarity: 30.56% Mismatches: 22
Query Match: 6.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1156 CAGGTCCAGCAATCCTACCCCTCGATGGATCCCGCGGGGTACCGAGCTCGAATTAGTCT 1097
Qy 21 CysTyrAspAsnGlyHisTyrGlnIleAsnGlnGlnTrpGluArg 36
Db 1096 GCGCGTCTTTCAGGGCTTCATCGACAGTCTGACACCGCTGGCGGCGT 1049

RESULT 7

AAx80497

ID AAX80497 standard; cDNA; 2385 BP.

AC AAX80497;

XX 26-AUG-1999 (first entry)

XX Streptokinase and maltose binding protein fusion protein encoding cDNA.

XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

XX nsk; rsk; bacterial; blood clot; thrombotic condition;

XX myocardial infarction; venous thrombosis; pulmonary embolism;

XX cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.

XX Streptococcus dysgalactiae subsp. equisimilis.

OS Synthetic.

XX WO9931247-A1.

XX 24-JUN-1999.

XX 15-DEC-1998; 98WO-US026694.

XX 15-DEC-1997; 97US-0069497P.

XX (HARD) HARVARD COLLEGE.

XX Reed GL;

XX WPI; 1999-395183/33.

XX P-FSDB; AAY24797.

XX N-terminally deleted streptokinase.

XX Example; Page 45-48; 73pp; English.

XX The present invention describes an isolated bacterial protein that

XX induces fibrin-dependent plasminogen activation in a pharmaceutical

XX composition for dissolving blood clots. Also described are: (1) a

XX composition comprising an isolated modified streptokinase, the

XX modification being removal of amino acid residues in the amino terminus;

CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes a streptokinase and maltose binding protein fusion protein from
CC an example of the present invention
XX
SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.15 Length: 2385
Score: 38.00 Matches: 15
Percent Similarity: 33.90% Conservative: 5
Best Local Similarity: 25.42% Mismatches: 35
Query Match: 6.33% Indels: 4
DB: 8 Gaps: 1

US-09-940-235-4 (1-259) x AAX80497 (1-2385)

Qy 14 ValSerGlnSerLysProGlyCysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGln 33
Db 933 GTTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAGAACGCCAGAAAGGTGAATCAT 992
Qy 34 TrpGluArgThrTyrLeuGlyAsnValLeuValCysThrCysTyrGlyGly----- 50
Db 993 GCGAAACATCCCGCAGATGCCCTTTCTGGTATGCCGTGCTGCTGATCAACGC 1052
Qy 51 ---SerArgGlyPheAsnCysGluSerLysProGluAlaGluGluThrCysPheAsp 68
Db 1053 CGCCAGCGTCTGCAGACTGTCGATGAAGCCCTGAAGAGCCGCGCAGACTAATTCGAG 1109

RESULT 8

AAx80497/c

ID AAX80497 standard; cDNA; 2385 BP.

XX AAX80497;

XX 26-AUG-1999 (first entry)

XX Streptokinase and maltose binding protein fusion protein encoding cDNA.

XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

XX nsk; rsk; bacterial; blood clot; thrombotic condition;

XX myocardial infarction; venous thrombosis; pulmonary embolism;

XX cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.

XX Streptococcus dysgalactiae subsp. equisimilis.

OS Synthetic.

XX WO9931247-A1.

XX 24-JUN-1999.

XX 15-DEC-1998; 98WO-US026694.

XX 15-DEC-1997; 97US-0069497P.

XX (HARD) HARVARD COLLEGE.

XX Reed GL;

XX WPI; 1999-395183/33.

```

DR P-PSDB; AAY24797.
XX
XX N-terminally deleted streptokinase.
XX
XX Example; Page 45-48; 73pp; English.
XX
CC The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes a streptokinase and maltose binding protein fusion protein from
CC an example of the present invention
XX
XX Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.15 Length: 2385
Score: 38.00 Matches: 11
Percent Similarity: 38.89% Conservative: 3
Best Local Similarity: 30.56% Mismatches: 22
Query Match: 6.33% Indels: 0
DB: 8 Gaps: 0

US-09-940-235-4 (1-259) x AAX80497 (1-2385)

QY 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1156 CAGGTCACAGATCTCTACCTCGATGATCCCGCGCGGTACCGAGTCGAATTAGTCT 1097
QY 21 CysTyrAspAsnGlyHisTyrGlnIleAsnGlnTrpGluArg 36
Db 1096 GCGCGCTCTTTCAGGGCTTCATCGACATCTGACAGCCGTCGGCGCGT 1049

RESULT 9
SEDEX/c SEDEXB 8931 bp DNA linear BCT 17-FEB-1997
LOCUS S.equisimilis dextb, abc, lrp, skc, rel genes and ORF1.
DEFINITION X72832
ACCESSION X72832
VERSION X72832.1 GI:407876
KEYWORDS abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan
1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel
gene; skc gene; streptokinase; stringent response-like protein.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 3621 to 6190)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
REFERENCE 2 (bases 1 to 4188; 5790 to 8931)
AUTHORS Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE Genetic organization of the streptokinase region of the
Streptococcus equisimilis H46A chromosome
JOURNAL Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
MEDLINE 94049672
PUBMED 8232196
REFERENCE 3 (bases 1 to 8931)
AUTHORS Malke,H
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
Jena University, Winzerlaer Str 10, 07708 Jena, FRG
COMMENT Related sequences: K02986, M19346, X13399 & X13400.
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/strain="H46A"
/isolate="human group C strain"
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/db_xref="taxon:119602"
/chromosome="streptokinase region"
/clone_lib="E.coli plasmid library containing subfragments
of the submitted seq:pSHD14/16, pSPV19, pSH2, pMF1,
pCWP73, pRH10, pWX4"
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ITSDEHAFVEARENPSPERYIWRDPNNILMSIFSGSAWELDEASGQYIHLFSK
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KQPDNLWENAHVRQKLYDMNFWIAKGI GGFMDVIDLGIKIPDSEITGNPRLHDYL
KEMNQATFGNHDVTGSETGWATPEIARQYSRPNKELSNVQFEHVGLQHKPNAPKW
DYABEADVPALKTFISKQWTELKLGEGNSLFWNHDLPRLVSIWNGDSIYREKSACA
LAILLMRGTPYIYQGEIGITMNTYPPKDLTEVDDIESLNKAKENGVPAARVMS
IRKVGNDARTPMWSKDTHAGSEAQETWLPVNPVQEIINVADALANODSIFTYTQQ
LIALRKQDWLVEADYVHLLPTADKVFAYQORQGEETVIVVNVSDQEQVFAKDLAGE
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/notes="Walker motif B"
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/notes="(+) frame shift mutation in H46A"
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/gene="abc"

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complement(2973..2976)
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AVRKIVNRIFFSDADGKMQNSIQDIKGSILSVSQFTLYADTKGNRPFTGAAPDMA
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6007..6009
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Pred. No.: 18.4 Length: 8931
Score: 38.00 Matches: 9
Percent Similarity: 42.86% Conservative: 0
Best Local Similarity: 42.86% Mismatches: 12
Query Match: 6.33% Indels: 0
DB: 4 Gaps: 0

US-09-940-235-4 (1-259) x SEDEXB (1-8931)

QY 65 ThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThrTyrGluArgPro 84
Db 7870 ACCAAATCAAGTCTTATACCACTGACGACGGCTTTGGTGTGTTATGTCGACCA 7811
QY 85 Lys 85
Db 7810 AAA 7808

RESULT 10
AAI16632
ID AAI16632 standard; DNA; 1242 BP.
XX
AC AAI16632;
XX
DT 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding DNA.
XX
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
KW serine protease; fibrin; blood clot; thrombolytic;
KW vascular thromboembolytic symptom; acute myocardial infarction;
KW fibrinolysis; resistance; ds.
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
FH Key Location/Qualifiers
FT CDS 1..1242
FT /*tag= a
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FT      /transl_except= (pos:40..42,aa:Asn)
FT      /note= "no stop codon given"
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PN      US5876999-A.
XX
XX
PD      02-MAR-1999.
XX
XX
PF      06-DEC-1995; 95US-00568393.
XX
XX
PR      06-DEC-1995; 95US-00568393.
XX
XX
PA      (NASC-) NAT SCI COUNCIL.
XX
XX
PI      Wu H;
XX
XX
DR      WPI: 1999-189643/16.
XX
XX
DR      P-PSDB; AAW94664.
XX
XX
XX      Mutant streptokinase polypeptide - useful as plasmin-resistant
XX      thrombolytic agent.
XX
XX      Claim 1; Col 7-10; 17pp; English.
XX
XX      The present invention describes a mutant streptokinase (SK) polypeptide
XX      in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
XX      segment of the corresponding native SK is replaced by another amino acid.
XX      The present sequence encodes native SK. SK is a secretory protein of
XX      haemolytic Streptococcus able to activate human plasminogen (HPLg) to
XX      plasmin (HPLm), which is a serine protease able to catalyse the
XX      hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
XX      agent in the treatment of vascular thromboembolytic symptoms such as
XX      acute myocardial infarction. Compared with wild-type SK, the K59E mutant
XX      is more resistant to degradation by human plasmin and is more effective
XX      both in acting as a fibrinolytic agent and in activating human plasminogen.
XX      (Updated on 17-OCT-2003 to standardise OS field)
XX
XX      Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.8 Length: 1242
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 6 Gaps: 2

US-09-940-235-4 (1-259) x AAX16632 (1-1242)
QY      44 ValCysThrCysTyrglyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
DB      1090 ATCATACCGTTTATATGGCAAGCGA-----CCCGAGGAGAG 1128
QY      64 GluThrCysPhe-----AspLysTyThr 71
DB      1129 AATGCTAGCTATCATTTAGCCTATGATATAAGATCGTTATACC 1170

RESULT 11
AAX80492
ID      AAX80492 standard; cDNA; 1242 BP.
XX
XX
AC      AAX80492;
XX
XX
DT      17-OCT-2003 (revised)
DT      26-AUG-1999 (first entry)
XX
XX
DE      Streptococcus equisimilis native streptokinase encoding cDNA.
XX
XX      Streptococcus streptokinase; fibrin-dependent plasminogen activator;
XX      nSK; rSK; bacterial; blood clot; thrombotic condition;
XX      myocardial infarction; venous thrombosis; pulmonary embolism;
XX      cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX
XX      Streptococcus dysgalactiae subsp. equisimilis.
XX
XX
XX      WO9931247-A1.
XX
XX      24-JUN-1999.
XX
XX      15-DEC-1998; 98WO-US026694.
XX
XX      15-DEC-1997; 97US-0069497P.
XX
XX      (HARD ) HARVARD COLLEGE.
XX
XX      Reed GL;
XX
XX      WPI: 1999-395183/33.
XX
XX      P-PSDB; AAY24794.
XX
XX      N-terminally deleted streptokinase.
XX
XX      Claim 44; Page 58-60; 73pp; English.
XX
XX      The present invention describes an isolated bacterial protein that
XX      induces fibrin-dependent plasminogen activation in a pharmaceutical
XX      composition for dissolving blood clots. Also described are: (1) a
XX      composition comprising an isolated modified streptokinase, the
XX      modification being removal of amino acid residues in the amino terminus;
XX      (2) a method for dissolving a blood clot in a subject, comprising
XX      administering to the subject a fibrin-dependent streptokinase protein; a
XX      nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
XX      expression vector comprising (1); and (4) a host cell transformed with
XX      the expression vector of (3). The pharmaceutical composition comprising a
XX      bacterial fibrin-dependent plasminogen activator is useful for dissolving
XX      blood clots in patients with a thrombotic condition, e.g. myocardial
XX      infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
XX      graft thrombosis and arterial thrombosis. The modified streptokinase can
XX      also be used in non-human mammals. Streptokinase activation of
XX      plasminogen is at least 10-fold, preferably 100-fold greater in the
XX      presence of fibrin than in the absence of fibrin. The modified
XX      streptokinase has at least one amino acid substitution that inactivates a
XX      substrate site for proteolytic cleavage. This reduces the rate of
XX      degradation of the streptokinase at least two-fold. The present sequence
XX      encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
XX      standardise OS field)
XX
XX      Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.8 Length: 1242
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 7 Gaps: 2

US-09-940-235-4 (1-259) x AAX80492 (1-1242)
QY      44 ValCysThrCysTyrglyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
DB      1090 ATCATACCGTTTATATGGCAAGCGA-----CCCGAGGAGAG 1128
QY      64 GluThrCysPhe-----AspLysTyThr 71
DB      1129 AATGCTAGCTATCATTTAGCCTATGATATAAGATCGTTATACC 1170

RESULT 12
us-09-211-542a-5
XX
XX
XX      Alignment Scores:
XX      Pred. No.: 8.8 Length: 1242
XX      Score: 33.50 Matches: 10
XX      Percent Similarity: 38.24% Conservative: 3
XX      Best Local Similarity: 29.41% Mismatches: 8
XX      Query Match: 5.58% Indels: 13
XX      DB: 9 Gaps: 2

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US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)
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Db 1090 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1128

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1129 AATGCTAGCTATCATTTAGCCTATGATAAAGATCGTTATACC 1170

RESULT 13
us-09-568-393b-1
Alignment Scores:
Pred. No.: 8.8 Length: 1242
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 10 Gaps: 2

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)
Qy 44 ValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
Db 1090 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1128

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1129 AATGCTAGCTATCATTTAGCCTATGATAAAGATCGTTATACC 1170

RESULT 14
I05204
LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1401)
Hagenson,M.J. and Stroman,D.W.
Yeast production of streptokinase
Patent: EP 0248227-A1 5 09-DEC-1987;
JOURNAL
FEATURES
source
1. .1401
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 9.86 Length: 1401
Score: 33.50 Matches: 10
Percent Similarity: 38.24% Conservative: 3
Best Local Similarity: 29.41% Mismatches: 8
Query Match: 5.58% Indels: 13
DB: 3 Gaps: 2

US-09-940-235-4 (1-259) x I05204 (1-1401)
Qy 44 ValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysProGluAlaGlu 63
Db 1099 ATCATAAACCGTTTATATGGCAAGCGA-----CCCCGAAGGAGAG 1137

Qy 64 GluThrCysPhe-----AspLysTyrThr 71
Db 1138 AATGTCAGCTATCATTTAGCCTATGATAAAGATCGTTATACC 1179

RESULT 15
AAAX16632/c
ID AAAX16632 standard; DNA; 1242 BP.
XX

```

```

AC AAAX16632;
XX
DT 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding DNA.
XX
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
KW serine protease; fibrin; blood clot; thrombolytic;
KW vascular thromboembolytic symptom; acute myocardial infarction;
KW fibrinolysis; resistance; ds.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
FH Key Location/Qualifiers
FT CDS 1..1242
FT /*tag= a
FT /transl_except= (pos:40..42,aa:Asn)
FT /note= "no stop codon given"
XX
PN US5876999-A.
XX
PD 02-MAR-1999.
XX
PF 06-DEC-1995; 95US-00568393.
XX
PR 06-DEC-1995; 95US-00568393.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Wu H;
XX
WPI: 1999-189643/16.
P-PSDB; AAW94664.
XX
PT Mutant streptokinase polypeptide - useful as plasmin-resistant
PT thrombolytic agent.
XX
PS Claim 1; Col 7-10; 17pp; English.
XX
CC The present invention describes a mutant streptokinase (SK) polypeptide
CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
CC segment of the corresponding native SK is replaced by another amino acid.
CC The present sequence encodes native SK. SK is a secretory protein of
CC haemolytic Streptococcus able to activate human plasminogen (HPLg) to
CC plasmin (HPLm), which is a serine protease able to catalyse the
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
CC agent in the treatment of vascular thromboembolytic symptoms such as
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
CC is more resistant to degradation by human plasmin and is more effective
CC both in acting as a fibrinolytic agent and in activating human plasminogen.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: 6 Gaps: 2

US-09-940-235-4 (1-259) x AAAX16632 (1-1242)
Qy 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db 581 ATGGTGTACCGATAGTAGTGTGTTTCAATAGCTTAGTCTTTGAGACCTGGTCTGAAA 522
Qy 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db 521 TCGTCATCAGGGTTTAAGGGAGTAAC----- 495

```

```
QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
   ||||| ||||| ||||| |||||
Db 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 16
ID AAX80492/c
XX AAX80492 standard; cDNA; 1242 BP.
AC AAX80492;
XX
DT 17-OCT-2003 (revised)
DT 26-AUG-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding cDNA.
XX
KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
KW nSK; rSK; bacterial; blood clot; thrombotic condition;
KW myocardial infarction; venous thrombosis; pulmonary embolism;
KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
PN WO931247-Al.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98WO-US026694.
XX
PR 15-DEC-1997; 97US-0069497P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Reed GL;
XX
DR WPI; 1999-395183/33.
DR P-PSDB; AAY24794.
XX
PT N-terminally deleted streptokinase.
XX
PS Claim 44; Page 58-60; 73pp; English.
XX
CC The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15

QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
   ||||| ||||| ||||| |||||
Db 581 ATGGTGTCCCGATAGCTAGTGTTCATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 522

RESULT 17
us-09-211-542a-5/c
Alignment Scores:
Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: Gaps: 2

US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)
QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
   ||||| ||||| ||||| |||||
Db 581 ATGGTGTCCCGATAGCTAGTGTTCATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 522

QY 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
   :||| :||| :||| :|||
Db 521 TCGTTCATCAGGGTTTAAGGGAGTAAAC----- 495

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
   ||||| ||||| ||||| |||||
Db 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 18
us-08-568-393b-1/c
Alignment Scores:
Pred. No.: 17.4 Length: 1242
Score: 28.50 Matches: 12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match: 4.75% Indels: 15
DB: Gaps: 2

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)
QY 5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
   ||||| ||||| ||||| |||||
Db 581 ATGGTGTCCCGATAGCTAGTGTTCATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 522

QY 23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
   :||| :||| :||| :|||
Db 521 TCGTTCATCAGGGTTTAAGGGAGTAAAC----- 495

QY 43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
   ||||| ||||| ||||| |||||
Db 494 -----TGTACAGTATATCCACATCAACAGATTTC 465

RESULT 19
I05204/c
LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
```

```

SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1401)
AUTHORS     Hagenson,M.J. and Stroman,D.W.
TITLE       Yeast production of streptokinase
JOURNAL     Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES    Location/Qualifiers
             source
               1..1401
               /organism="unknown"
               /mol_type="unassigned DNA"

Alignment Scores:
Pred. No.:      18.1      Length:      1401
Score:          28.50     Matches:      12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match:    4.75%     Indels:      15
DB:             3        Gaps:         2

US-09-940-235-4 (1-259) x I05204 (1-1401)

Qy      5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db      590 ATGGTGTACCCGATAGCTAGTGTTCATATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 531
Qy      23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db      530 TCGTCATCAGGGTTTAAGGGAGTAAAC-----
Qy      43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
Db      503 -----TGTACAGTATATTCACATCAACAGATTTC 474

RESULT 20
STRSKC/c  LOCUS
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION K02986
VERSION   K02986.1 GI:153808
KEYWORDS Streptococcus dysgalactiae subsp. equisimilis
SOURCE    Streptococcus dysgalactiae subsp. equisimilis
ORGANISM  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
           Streptococcus.
REFERENCE 1 (bases 1 to 2568)
AUTHORS   Malke,H., Roe,B. and Ferretti,J.J.
TITLE     Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL   Gene 34 (2-3), 357-362 (1985)
MEDLINE   85232082
PUBMED    2989113
COMMENT   Original source text: S.equisimilis (strain H46A) DNA, clone pMF5.
           Draft entry and hard copy of sequence for [1] kindly provided by
           J.J.Ferretti, 03-SEP-1985.
           The -35 and -10 regions are located at positions 760-765 and
           781-786 respectively and an SD sequence at 808-813. Downstream
           from the coding region inverted repeats (positions 2176-2190 and
           2203-2217) are thought to function as transcription terminators.
           The nucleotide sequence of skc does not support the hypothesis that
           the gene has evolved by duplication and fusion, as suggested by
           internal two-fold AA homologies of its product.

FEATURES    Location/Qualifiers
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             /db_xref="taxon:119602"
             794..>2141
             /product="skc mRNA"
             819..2141
             /notes="prestreptokinase"
             /codon_start=1
             /transl_table=11

sig_peptide
mat_peptide

Alignment Scores:
Pred. No.:      19.9      Length:      2568
Score:          28.50     Matches:      12
Percent Similarity: 34.62% Conservative: 6
Best Local Similarity: 23.08% Mismatches: 19
Query Match:    4.75%     Indels:      15
DB:             5        Gaps:         2

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy      5 MetValGlnProGlnSerProVal-----AlaValSerGlnSerLysProGlyCysTyr 22
Db      1477 ATGGTGTACCCGATAGCTAGTGTTCATATAGCTTAGTATCTTTGAGACCTGGTCTGAAA 1418
Qy      23 AspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGlyAsnVal 42
Db      1417 TCGTCATCAGGGTTTAAGGGAGTAAAC-----
Qy      43 LeuValCysThrCysTyrGlyGlySerArgGlyPhe 54
Db      1390 -----TGTACAGTATATTCACATCAACAGATTTC 1361

Search completed: December 6, 2004, 15:00:58
Job time : 5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 14:53:42 ; Search time 1 Seconds
(without alignments)
0.613 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 500
Sequence: 1 QAQKWQPQSPVAVSQSPG.....SMWDTCTIGAGRGISCTI 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12 seqs, 5782 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 12 summaries

Database :
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2: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aar63120.geneseqp1990a
3: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aaw94664.geneseqp1990a
4: /staff_overflow/sdavid-tmp/dec04/swope235/pep/aay01556.geneseqp1990a
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12: /staff_overflow/sdavid-tmp/dec04/swope235/pep/us-09-211-542a-2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	5.6	414	1	AAR10194
2	33.5	5.6	414	2	AAR63120
3	33.5	5.6	414	3	AAR94664
4	33.5	5.6	414	4	AAY01556
5	33.5	5.6	414	5	AAY24794
6	33.5	5.6	414	7	pct-us93-09502-1
7	33.5	5.6	414	8	us-08-128-299-1
8	33.5	5.6	414	10	us-09-211-542a-6
9	33.5	5.6	440	9	STREP STREQ
10	33.5	5.6	440	11	us-08-560-098a-52
11	33.5	5.6	795	6	AAY24797
12	33.5	5.6	795	12	us-09-211-542a-2

ALIGNMENTS

RESULT 1
AAR10194
ID AAR10194 standard; protein; 414 AA.

XX

AC AAR10194;
XX 28-MAR-1991 (first entry)
XX Streptokinase encoded by synthetic gene.
XX streptokinase; thrombolytic agent; myocardial infarction.
XX Synthetic.
XX EP407942-A.
XX 16-JAN-1991.
XX 11-JUL-1989; 89JP-00179432.
XX 11-JUL-1989; 89JP-00179432.
XX 27-NOV-1989; 89JP-00307957.
XX 11-APR-1990; 90JP-00096830.
XX (SAKA) OTSUKA PHARM FACTOR.
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX WPI; 1991-016179/03.
XX N-PSDB; AAQ10230.
XX Synthetic gene encoding streptokinase - scale, high purity prodn. of
XX streptokinase used as a thrombolytic agent.
XX Claim 1; Page 51; 76pp; English.
XX Streptokinase and its derivatives can be produced in large quantities
XX with high purity for use as thrombolytic agents in patients with lung
XX thrombus or myocardial infarction. See also AAR10195-R10200
XX Sequence 414 AA;
XX Query Match 5.6%; Score 33.5; DB 1; Length 414;
XX Best Local Similarity 29.4%; Pred. No. 0;
XX Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
Oy 44 VCTCYGSGRGNCEKPEAETCF-----DKYT 71
Db 364 IITVYMKR-----PEGENASVHLAYDKDRYT 390
RESULT 2
AAR63120
ID AAR63120 standard; protein; 414 AA.
XX AC AAR63120;
XX 16-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-NOV-1994 (first entry)
XX Streptokinase.
XX Streptokinase; SK; Streptococcus equisimilis; plasminogen;
XX myocardial infarction.
XX Streptococcus dysgalactiae subsp. equisimilis.
XX Key Location/Qualifiers
XX Region 1..352
XX /note= "claim 3, see CC"
XX Region 14..414
XX /note= "claim 1, see CC"
XX Region 120..352
XX /note= "claim 3, see CC"
XX Region 244..414
XX /note= "claim 3, see CC"

FT	Region	244..352 /notes="Claim 2, see CC"
XX		
XX		
PN	WO9407992-A1.	
XX		
PD	14-APR-1994.	
XX		
XX		
PF	05-OCT-1993;	93WO-US009502.
XX		
PR	05-OCT-1992;	92US-00956692.
XX		
PR	29-SEP-1993;	93US-00128299.
XX		
XX		
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
PA	(HARD) HARVARD COLLEGE.	
XX		
PI	Reed GL;	
XX		
DR	WPI; 1994-135561/16.	
XX		
PT	DNA encoding a polypeptide which binds to plasminogen and corresponds to	
XX		
PT	region of streptokinase - useful to detect plasminogen in a sample and to	
PT	treat myocardial infarction.	
XX		
PS	Disclosure; Page 40-41; 62pp; English.	
XX		
CC	Nucleic acid comprising a sequence encoding amino acids 14-414 of	
CC	streptokinase, which binds to plasminogen and does not have a sequence	
CC	comprising amino acids 60-414 is new. The polypeptide pref. comprises	
CC	amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003	
CC	to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 414 AA;	
	Query Match	5.6%; Score 33.5; DB 2; Length 414;
	Best Local Similarity	29.4%; Pred.No. 0;
	Matches	10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
QY	44 VCTCYGSGRGFNCESKPEAEETCF-----DKYT 71	
	: : : : : : : : : : : : : : : : :	
DB	364 IITVMGKR-----PEGENASYHLAYDKDRT 390	
	RESULT 3	
	AAW94664	
ID	AAW94664 standard; protein; 414 AA.	
AC	AAW94664;	
XX		
DT	17-OCT-2003 (revised)	
XX		
DT	04-MAY-1999 (first entry)	
XX		
DE	Streptococcus equisimilis native streptokinase.	
XX		
KW	Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;	
KW	plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;	
KW	serine protease; fibrin; blood clot; thrombolytic;	
KW	vascular thromboembolytic symptom; acute myocardial infarction;	
KW	fibrinolysis; resistance.	
OS	Streptococcus dysgalactiae subsp. equisimilis.	
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 14	
FT	/note= "encoded by ACC"	
XX		
PN	US5876999-A.	
XX		
PD	02-MAR-1999.	
XX		
XX		
PF	06-DEC-1995;	95US-00568393.
XX		
PR	06-DEC-1995;	95US-00568393.
XX		

PA	(NASC-) NAT SCI COUNCIL.	
XX		
PI	Wu H;	
XX		
DR	WPI; 1999-189643/16.	
DR	N-PSDB; AAXI6632.	
XX		
FT	Mutant streptokinase polypeptide - useful as plasmin-resistant	
PT	thrombolytic agent.	
XX		
PS	Claim 1; Col 7-10; 17pp; English.	
XX		
CC	The present invention describes a mutant streptokinase (SK) polypeptide	
CC	in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61	
CC	segment of the corresponding native SK is replaced by another amino acid.	
CC	The present sequence represents native SK. SK is a secretory protein of	
CC	haemolytic Streptococcus able to activate human plasminogen (HPlg) to	
CC	plasmin (HPIm) which is a serine protease able to catalyse the	
CC	hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic	
CC	agent in the treatment of vascular thromboembolytic symptoms such as	
CC	acute myocardial infarction. Compared with wild-type SK, the K59E mutant	
CC	is more resistant to degradation by human plasmin and is more effective	
CC	both in acting as a fibrolytic agent and in activating human plasminogen.	
CC	(Updated on 17-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 414 AA;	
	Query Match	5.6%; Score 33.5; DB 3; Length 414;
	Best Local Similarity	29.4%; Pred.No. 0;
	Matches	10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;
QY	44 VCTCYGSGRGFNCESKPEAEETCF-----DKYT 71	
	: : : : : : : : : : : : : : : : :	
DB	364 IITVMGKR-----PEGENASYHLAYDKDRT 390	
	RESULT 4	
	AAW01556	
ID	AAW01556 standard; peptide; 414 AA.	
XX		
AC	AAW01556;	
XX		
DT	17-OCT-2003 (revised)	
DT	18-JUN-1999 (first entry)	
XX		
DE	Native streptokinase protein sequence.	
XX		
KW	Antigenic peptide; streptokinase; streptokinase-specific antibody;	
KW	thrombolytic activity; thrombolytic therapy; glomerulonephritis;	
KW	rheumatic fever.	
XX		
OS	Streptococcus dysgalactiae subsp. equisimilis.	
XX		
PN	WO9908698-A1.	
XX		
XX		
PD	25-FEB-1999.	
XX		
PF	18-AUG-1998;	98WO-US017114.
XX		
PR	18-AUG-1997;	97US-0055911P.
XX		
PA	(HARD) HARVARD COLLEGE.	
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
PI	Reed GL, Parhami-Seren B;	
DR	WPI; 1999-190113/16.	
XX		
XX	New polypeptides which bind streptokinase-specific antibodies - useful in	
PT	thrombolytic therapy.	
XX		
PS	Disclosure; Page 12; 44pp; English.	
XX		

CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC represents native streptokinase (nsk). (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 414 AA;

```

Query Match          5.6%; Score 33.5; DB 5; Length 414;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGGSGFNCESKPEAETCF-----DKYTT 71
   ||| ||| ||| | : |||
DB 364 IITVYMGKR-----PEGENASYHLAYDKDRYT 390

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Query Match	5.6%;	Score 33.5;	DB 7;	Length 414;
Best Local Similarity	29.4%;	Pred. No. 0;		

vaccines 10; conservative 3; mismatches 0; under 10; cups 2

VY : ||||| :
49 VCICGACRNCGRK EALFIC

Db IITVNGKR-----PEGENASYHLYDKORYT 390

us-08-128-299-1

Query Match	5.6%;	Score 33.5;	DB 8;	Length 414;
Best Local Similarity	29.4%;	Pred. No. 0;		

[illegible][illegible]

.....

RESULT 8

[illegible]

Best Local Similarity 29.4%; Pred. No. 0;

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364 IITVNGKR-----PEGENASYHLAYDKORYT 390

STRP STREQ

AC P00779;

DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Streptokinase C precursor.
GN	Name=skc;
OS	Streptococcus equisimilis.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=119602;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=H46A;
RX	MEDLINE=85232082; PubMed=2989113;
RA	Malke H., Roe B., Ferretti J.J.;
RT	"Nucleotide sequence of the streptokinase gene from Streptococcus

Query Match 5.6%; Score 33.5; DB 6; Length 795;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGFNCESKPEAEETCF-----DKYT 71
DB 745 IITVYMGKR-----PEGENASYHLAYDKDRYT 771

RESULT 12
us-09-211-542a-2

Query Match 5.6%; Score 33.5; DB 12; Length 795;
Best Local Similarity 29.4%; Pred. No. 0;
Matches 10; Conservative 3; Mismatches 8; Indels 13; Gaps 2;

QY 44 VCTCYGSGRGFNCESKPEAEETCF-----DKYT 71
DB 745 IITVYMGKR-----PEGENASYHLAYDKDRYT 771

Search completed: December 6, 2004, 14:53:45
Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2004, 15:02:16 ; Search time 2 Seconds
(without alignments)
2.629 Million cell updates/sec

Title: US-09-940-235-4
Perfect score: 627
Sequence: 1 PIAKCFDHAAGTSYVVGST.....ERHTSVQTTSGSGPFTDVR 110

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 10 seqs, 23900 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 20 summaries

Command line parameters:
-MODEL=frame_p2n.model -DEV=soft -Q=Pending Patents AA Main:US-09-940-235-4
-DB=- -SUFFIX=ptc -OUT=align4_150_259_seq -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=150 -END=259 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=20
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6
-NO_XLPXY -NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: /staff_overflow/sdavid-tmp/dec04/swope235/seq/ar143998.gb.pat.*
2: /staff_overflow/sdavid-tmp/dec04/swope235/seq/e03308.gb.pat.*
3: /staff_overflow/sdavid-tmp/dec04/swope235/seq/105204.gb.pat.*
4: /staff_overflow/sdavid-tmp/dec04/swope235/seq/sedexb.gb.pat.*
5: /staff_overflow/sdavid-tmp/dec04/swope235/seq/atrksc.gb.pat.*
6: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa16632.geneseq1990e
7: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa80497.geneseq1990e
8: /staff_overflow/sdavid-tmp/dec04/swope235/seq/aa80497.geneseq1990e
9: /staff_overflow/sdavid-tmp/dec04/swope235/seq/us-09-211-542a-5.*
10: /staff_overflow/sdavid-tmp/dec04/swope235/seq/us-08-568-393b-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41	6.5	8931	4 SEDXB	ACCESSION:X72832
2	39	6.2	8931	4 SEDXB	ACCESSION:X72832
C 3	33.5	5.3	1242	6 AAX16632	Streptococcus equi
C 4	33.5	5.3	1242	7 AAX80492	Streptococcus equi
C 5	33.5	5.3	1242	9 us-09-211-542a-5	
C 6	33.5	5.3	1242	10 us-08-568-393b-1	
C 7	33.5	5.3	1401	3 I05204	ACCESSION:I05204
C 8	33.5	5.3	2385	1 AR143998	ACCESSION:AR143998
C 9	33.5	5.3	2385	8 AAX80497	Streptokinase and
C 10	33.5	5.3	2568	5 STRSKC	ACCESSION:K02986
11	33	5.3	2385	1 AR143998	ACCESSION:AR143998

12 33 5.3 2385 8 AAX80497 Streptokinase and
13 31.5 5.0 1242 6 AAX16632 Streptococcus equi
14 31.5 5.0 1242 7 AAX80492 Streptococcus equi
15 31.5 5.0 1242 9 us-09-211-542a-5
16 31.5 5.0 1242 10 us-08-568-393b-1
17 31.5 5.0 1242 2 E03308 ACCESSION:E03308
18 31.5 5.0 1401 3 I05204 ACCESSION:I05204
19 31.5 5.0 2568 5 STRSKC ACCESSION:K02986
c 20 27 4.3 1262 2 E03308 ACCESSION:E03308

ALIGNMENTS

RESULT 1
SEDEXB/c
LOCUS SEDXB 8931 bp DNA linear BCT 17-FEB-1997
DEFINITION S. equisimilis dexb, abc, lrp, skc, rel genes and ORF1.
ACCESSION X72832
VERSION X72832.1 GI:407876
KEYWORDS abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan 1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel gene; skc gene; streptokinase; stringent response-like protein.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 3621 to 6190)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
REFERENCE 2 (bases 1 to 4188; 5790 to 8931)
AUTHORS Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE Genetic organization of the streptokinase region of the Streptococcus equisimilis H46A chromosome
Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
JOURNAL 94049672
MEDLINE 8232196
PUBMED
REFERENCE 3 (bases 1 to 8931)
AUTHORS Malke,H.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology, Jena University, Winzerlaer Str 10, 07708 Jena, FRG
COMMENT Related sequences: K02986, M19346, X13399 & X13400.
FEATURES
source
1. .8931
/organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
/strain="H46A"
/isolate="human group C strain"
/sub_species="equisimilis"
/db_xref="taxon:119602"
/clone_lib="E.coli plasmid library containing subfragments of the submitted seq:PSHD14/16, pSPV19, pSH2, pMFI, pCWP73, pRH10, pWX4"
complement (89. .1761)
/genes="dexB"
complement (89. .115)
/genes="dexB"
/notes="hairpin loop"
complement (136. .1749)
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/codon_start=1
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/product="glucan 1,6-alpha-glucosidase"
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/db_xref="GI:407877"
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/db_xref="Swiss-Prot:Q59905"


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Percent Similarity: 40.43% Conservative: 8
Best Local Similarity: 23.40% Mismatches: 14
Query Match: 6.54% Indels: 14
DB: 4 Gaps: 2

US-09-940-235-4 (1-259) x SEDEXB (1-8931)

Qy 213 AspThrTrpSerIysAspAsnArgGlyAsnLeuGlnCysIleCys----- 229
Db 3092 GAAGTTTGGTCG-----CTTGTCTCTGTTTGAAGC 3060
Qy 230 -----ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThr 247
Db 3059 GCTGTTTTGTGACATAAAGCATCAAAAAATGTCAGCGGTGCTTAGCGTTGCAGTCA 3000

Qy 248 ThrSerSerGlySerGlyPro 254
Db 2999 GCTAGAAAGCTGCTGCGCCA 2979

RESULT 2
LOCUS SEDEXB 8931 bp DNA linear BCT 17-FEB-1997
DEFINITION S.equisimilis dexb, abc, lrp, skc, rel genes and ORF1.
ACCESSION X72832
VERSION X72832.1 GI:407876
KEYWORDS abc gene; ABC transporter; dexB gene; dextran glucosidase; glucan
1,6-alpha-glucosidase; leucine rich protein; LRP gene; ORF1; rel
gene; skc gene; streptokinase; stringent response-like protein.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 3621 to 6190)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
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PUBMED 2989113
REFERENCE 2 (bases 1 to 4188; 5790 to 8931)
AUTHORS Mechold,U., Steiner,K., Vettermann,S. and Malke,H.
TITLE Genetic organization of the streptokinase region of the
Streptococcus equisimilis H46A chromosome
JOURNAL Mol. Gen. Genet. 241 (1-2), 129-140 (1993)
MEDLINE 94049672
PUBMED 8232196
REFERENCE 3 (bases 1 to 8931)
AUTHORS Malke,H.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1993) H. Malke, Institute for Molecular Biology,
Jena University, Winzerlaer Str 10, 07708 Jena, FRG
COMMENT Related sequences: K02986, M19346, X13399 & X13400.
FEATURES
source
1..8931
/organism="Streptococcus dysgalactiae subsp. equisimilis"
/mol_type="genomic DNA"
/strain="H46A"
/isolate="human group C strain"
/sub_species="equisimilis"
/db_xref="taxon:119602"
/chromosomes="streptokinase region"
/clone_lib="E.coli plasmid library containing subfragments
of the submitted seq:psHD14/16, pSPV19, pSH2, pMPL,
pCWP73, pRH10, pWX4"
complement(89..1761)
/gene="dexB"
complement(89..115)
/terminator
/gene="dexB"
/note="hairpin loop"
complement(136..1749)
/genes="dexB"
/EC_number="3.2.1.70"
/codon_start=1

/transl_table=11
/product="glucan 1,6-alpha-glucosidase"
/protein_id="CAA51348.1"
/db_xref="GI:407877"
/db_xref="GOA:Q59905"
/db_xref="Swiss-Prot:Q59905"
/translation="MQQWVHKATIIQIYPRSPKDTSGNGIGDKLGITSDLYLQKLG
ITAIWLSPPVYQSPMDNDGYDISDYEAIAEYVGNMDDMLAAANERGIKIMDLVNV
KPDENHAFVEARENPNSPRDYIMRDEPNNLMSIFSGAWELDEASGVYHLFSG
KQDLNENAHVRQKIYDMNFWIAKGIGGFRMDVILIGKIPDSEITGNRPRLHDYL
KENQATFGNHDVMTVGETGATPEIAROYSRPENKELSMVFQFEHVGLQKPNAPKW
DYAELDVPALKTIYFQKQTEKLKLGEGNSLFWNNHDLPRVLSIWNDSIYREKSAKA
LAILLHMRTPIYIQGEEIGMNTYPPFDLDEVDDIESLNAYKEAMENGVAPKVMSS
IRKVGDNARTPMQSKDTHAGFSEAQETWLPVNPYQEIINVDALANGQDSIFVYQO
LIALRKQDWLVEADYHLLPTADKFAFAYQRFQGETTYVIVVNSDQEQVFAKOLAGAE
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RBS complement(1757..1761)
/gene="dexB"
complement(1780..3051)
/gene="abc"
terminator complement(1780..1810)
/gene="abc"
/note="hairpin loop"
misc_feature complement(2482..2499)
/gene="abc"
CDS /note="Walker motif B"
complement(2633..2965)
/gene="abc"
/codon_start=1
/transl_table=11
/product="ABC transporter"
/protein_id="CAA51349.1"
/db_xref="GI:600072"
/db_xref="GOA:Q54086"
/db_xref="TrEMBL:Q54086"
/translation="MVLENLNIHYKKYVNTTHYAVEDFDLIDIKKEFIYFVGPSCGK
STLRMTAGLEDISEGELKIDGEVVDKSPDRDIAMVFQNYALYPHMTYVNNAFGL
KLRYKKR"
misc_feature complement(2644)
/gene="abc"
/note="(+) frame shift mutation in H46A"
misc_feature complement(2828..2854)
/gene="abc"
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RBS complement(2973..2976)
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QMTAGLEVILPISITQTAFRCQATSIKVLRSLEGLPTLESDFGLATMFVGNAMYQ
VAAGTLRECFEEECOLLTAYLKQKSGGKLLTFAEVLMLWSILSHQSFPALTQFQHFILN
PQSDMADVHVALSEHGNLVQTAQRLYIHNSLQYKLDKFAQQSGSLHLKQLDLDLAFAY

```


CC agent in the treatment of vascular thromboembolytic symptoms such as
 CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
 CC is more resistant to degradation by human plasmin and is more effective
 CC both in acting as a fibrolytic agent and in activating human plasminogen.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 6 Gaps: 1

US-09-940-235-4 (1-259) x AAX16632 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 4

ID AAX80492/c
 XX AAX80492 standard; cDNA; 1242 BP.
 AC AAX80492;
 XX
 XX 17-OCT-2003 (revised)
 DT 26-AUG-1999 (first entry)
 XX
 XX Streptococcus equisimilis native streptokinase encoding cDNA.
 DE
 XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
 KW nSK; rSK; bacterial; blood clot; thrombotic condition;
 KW myocardial infarction; venous thrombosis; pulmonary embolism;
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
 XX
 XX Streptococcus dysgalactiae subsp. equisimilis.
 OS
 XX WO931247-A1.
 PN
 XX 24-JUN-1999.
 PD
 XX 15-DEC-1998; 98WO-US026694.
 PF
 XX 15-DEC-1997; 97US-0069497P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Reed GL;
 PI
 XX WPI: 1999-395183/33.
 DR P-PSDB; AAY24794.
 DR
 XX N-terminally deleted streptokinase.
 PT
 XX Claim 44; Page 58-60; 73pp; English.
 PS
 XX The present invention describes an isolated bacterial protein that
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical
 CC composition for dissolving blood clots. Also described are: (1) a
 CC composition comprising an isolated modified streptokinase, the
 CC modification being removal of amino acid residues in the amino terminus;
 CC (2) a method for dissolving a blood clot in a subject, comprising
 CC administering to the subject a fibrin-dependent streptokinase protein; a
 CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
 CC expression vector comprising (1); and (4) a host cell transformed with
 CC the expression vector of (3). The pharmaceutical composition comprising a

CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
 CC blood clots in patients with a thrombotic condition, e.g. myocardial
 CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
 CC graft thrombosis and arterial thrombosis. The modified streptokinase can
 CC also be used in non-human mammals. Streptokinase activation of
 CC plasminogen is at least 10-fold, preferably 100-fold greater in the
 CC presence of fibrin than in the absence of fibrin. The modified
 CC streptokinase has at least one amino acid substitution that inactivates a
 CC substrate site for proteolytic cleavage. This reduces the rate of
 CC degradation of the streptokinase at least two-fold. The present sequence
 CC encodes native streptokinase (nSK). (Updated on 17-OCT-2003 to
 CC standardise OS field)

XX Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 7 Gaps: 1

US-09-940-235-4 (1-259) x AAX80492 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 5

us-09-211-542a-5/c

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 9 Gaps: 1

US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

Db 477 ATCAACAGATTTCGCTTGGTTTGTATGGT 447

RESULT 6

us-08-568-393b-1/c

Alignment Scores:
 Pred. No.: 2.19 Length: 1242
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservatives: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 10 Gaps: 1

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValaspCysThr----- 183
 |||||
 Db 537 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGGAGTAAACTGTACAGTATATTCAC 478
 |||||

Qy 184 -----CysLeuGly 186
 |||||

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Db 477 ATCAACAGATTCGCTTGGTTTGTATTGGT 447
RESULT 7
LOCUS I05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1401)
AUTHORS Hagenson,M.J. and Stroman,D.W.
TITLE Yeast production of streptokinase
JOURNAL Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES
location/Qualifiers
1..1401
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 2.98 Length: 1401
Score: 33.50 Matches: 10
Percent Similarity: 41.94% Conservative: 3
Best Local Similarity: 32.26% Mismatches: 6
Query Match: 5.34% Indels: 12
DB: 3 Gaps: 1

US-09-940-235-4 (1-259) x I05204 (1-1401)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183
Db 546 GAGACCTGCTCTGAATCGTCATCAGGGTTTAGGGGAGTAACGTACAGTATATCCAC 487
Qy 184 -----CysLeuGly 186
Db 486 ATCAACAGATTCGCTTGGTTTGTATTGGT 456

RESULT 8
LOCUS AR143998/2385 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210667.
ACCESSION AR143998
VERSION AR143998.1 GI:15105865
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2385)
AUTHORS Reed,G.L.
TITLE Bacterial fibrin-dependent plasminogen activator
JOURNAL Patent: US 6210667-A 1 03-APR-2001;
FEATURES
location/Qualifiers
1..2385
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 10 Length: 2385
Score: 33.50 Matches: 10
Percent Similarity: 41.94% Conservative: 3
Best Local Similarity: 32.26% Mismatches: 6
Query Match: 5.34% Indels: 12
DB: 1 Gaps: 1

US-09-940-235-4 (1-259) x AR143998 (1-2385)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183
Db 1680 GAGACCTGCTCTGAATCGTCATCAGGGTTTAGGGGAGTAACGTACAGTATATCCAC 1621
Qy 184 -----CysLeuGly 186
```

```
Db 1620 ATCAACAGATTCGCTTGGTTTGTATTGGT 1590
RESULT 9
LOCUS AAX80497/c
ID AAX80497 standard; cDNA; 2385 BP.
XX AC AAX80497;
XX 26-AUG-1999 (first entry)
XX Streptokinase and maltose binding protein fusion protein encoding cDNA.
XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
XX nSK; rSK; bacterial; blood clot; thrombotic condition;
XX myocardial infarction; venous thrombosis; pulmonary embolism;
XX cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX Streptococcus dysgalactiae subsp. equisimilis.
OS Synthetic.
XX WO9931247-A1.
XX 24-JUN-1999.
XX 15-DEC-1998; 98WO-US026694.
XX 15-DEC-1997; 97US-0069497P.
XX (HARD ) HARVARD COLLEGE.
XX Reed GL;
XX WPI; 1999-395183/33.
XX P-PSDB; AAY24797.
XX N-terminally deleted streptokinase.
XX Example; Page 45-48; 73pp; English.
XX The present invention describes an isolated bacterial protein that
XX induces fibrin-dependent plasminogen activation in a pharmaceutical
XX composition for dissolving blood clots. Also described are: (1) a
XX composition comprising an isolated modified streptokinase, the
XX modification being removal of amino acid residues in the amino terminus;
XX (2) a method for dissolving a blood clot in a subject, comprising
XX administering to the subject a fibrin-dependent streptokinase protein; a
XX nucleic acid (I) encoding a modified bacterial streptokinase; (3) an
XX expression vector comprising (I); and (4) a host cell transformed with
XX the expression vector of (3). The pharmaceutical composition comprising a
XX bacterial fibrin-dependent plasminogen activator is useful for dissolving
XX blood clots in patients with a thrombotic condition, e.g. myocardial
XX infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
XX graft thrombosis and arterial thrombosis. The modified streptokinase can
XX also be used in non-human mammals. Streptokinase activation of
XX plasminogen is at least 10-fold, preferably 100-fold greater in the
XX presence of fibrin than in the absence of fibrin. The modified
XX streptokinase has at least one amino acid substitution that inactivates a
XX substrate site for proteolytic cleavage. This reduces the rate of
XX degradation of the streptokinase at least two-fold. The present sequence
XX encodes a streptokinase and maltose binding protein fusion protein from
XX an example of the present invention
SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 10 Length: 2385
Score: 33.50 Matches: 10
Percent Similarity: 41.94% Conservative: 3
Best Local Similarity: 32.26% Mismatches: 6
Query Match: 5.34% Indels: 12
DB: 8 Gaps: 1
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US-09-940-235-4 (1-259) x AAX80497 (1-2385)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183
 Db 1680 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGAGTAACACTGTACAGTATATCCAC 1621

Qy 184 -----CysLeuGly 186
 Db 1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590

RESULT 10
 STRSKC/c
 LOCUS STRSKC 2568 bp DNA linear BCT 26-APR-1993
 DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
 ACCESSION K02986
 VERSION K02986.1 GI:153808
 KEYWORDS streptokinase.
 SOURCE Streptococcus dysgalactiae subsp. equisimilis
 ORGANISM Streptococcus dysgalactiae subsp. equisimilis
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE 1 (bases 1 to 2568)
 AUTHORS Malke, H., Roe, B. and Ferretti, J.J.
 TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
 JOURNAL Gene 34 (2-3), 357-362 (1985)
 MEDLINE 85232082
 PUBMED 2989113

COMMENT
 Original source text: S. equisimilis (strain H46A) DNA, clone pMF5. Draft entry and hard copy of sequence for [1] kindly provided by J.J. Ferretti, 03-SEP-1985.
 The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.
 Location/Qualifiers

FEATURES
 source 1..2568
 /organism="Streptococcus dysgalactiae subsp. equisimilis"
 /mol_type="genomic DNA"
 /db_xref="taxon:119602"
 794..>2141
 /product="skc mRNA"
 819..2141
 /note="prestreptokinase"
 /codon_start=1
 /transl_table=1
 /protein_id="AAA26974.1"
 /db_xref="GI:153809"
 translation="MKNYLSPGMFALLPALTFTGVNSVQALGPWLLDRPSVNSOLVSVAGTVEGTNQDISKFEIDLTSPAGGKTEQGLSPKKEFPATDSGAMSHKLEKADLLAQEQLIANHNDNDYFEVIDFASDATITDRNGKVFYFADKDGSVLPTQPVQEFLLSGHVRPYKPKPTIQNKAQSVDEYTVQFTPLNPDFFRPGKDTKLKLTLAGIDTTSQVELLAQSLINKNKAQSVYIYERDSIVTHNDNIFRTILPMDOEFTYRVKNRQAYRINKSGNEEINNTDLISEKYVLKKEGKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLTASERNLFDRLYDPRKALLYNLDLAFGIMDYTLTKGVNDHDDTNRILTYMGKREGENASVHLADKDRYTEEREVSYLRYTGTIPDPNDK"

sig_peptide 819..896
 /note="streptokinase signal peptide"
 mat_peptide 897..2138
 /product="streptokinase"

Alignment Scores:
 Pred. No.: 11.5 Length: 2568
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservative: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 5 Gaps: 1

US-09-940-235-4 (1-259) x STRSKC (1-2568)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183
 Db 1680 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGAGTAACACTGTACAGTATATCCAC 1621

Qy 184 -----CysLeuGly 186
 Db 1620 ATCAACAGATTTCGCTGGTTTGTATTGGT 1590

RESULT 10
 STRSKC/c
 LOCUS STRSKC 2568 bp DNA linear BCT 26-APR-1993
 DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
 ACCESSION K02986
 VERSION K02986.1 GI:153808
 KEYWORDS streptokinase.
 SOURCE Streptococcus dysgalactiae subsp. equisimilis
 ORGANISM Streptococcus dysgalactiae subsp. equisimilis
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE 1 (bases 1 to 2568)
 AUTHORS Malke, H., Roe, B. and Ferretti, J.J.
 TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
 JOURNAL Gene 34 (2-3), 357-362 (1985)
 MEDLINE 85232082
 PUBMED 2989113

COMMENT
 Original source text: S. equisimilis (strain H46A) DNA, clone pMF5. Draft entry and hard copy of sequence for [1] kindly provided by J.J. Ferretti, 03-SEP-1985.
 The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators. The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.
 Location/Qualifiers

FEATURES
 source 1..2568
 /organism="Streptococcus dysgalactiae subsp. equisimilis"
 /mol_type="genomic DNA"
 /db_xref="taxon:119602"
 794..>2141
 /product="skc mRNA"
 819..2141
 /note="prestreptokinase"
 /codon_start=1
 /transl_table=1
 /protein_id="AAA26974.1"
 /db_xref="GI:153809"
 translation="MKNYLSPGMFALLPALTFTGVNSVQALGPWLLDRPSVNSOLVSVAGTVEGTNQDISKFEIDLTSPAGGKTEQGLSPKKEFPATDSGAMSHKLEKADLLAQEQLIANHNDNDYFEVIDFASDATITDRNGKVFYFADKDGSVLPTQPVQEFLLSGHVRPYKPKPTIQNKAQSVDEYTVQFTPLNPDFFRPGKDTKLKLTLAGIDTTSQVELLAQSLINKNKAQSVYIYERDSIVTHNDNIFRTILPMDOEFTYRVKNRQAYRINKSGNEEINNTDLISEKYVLKKEGKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLTASERNLFDRLYDPRKALLYNLDLAFGIMDYTLTKGVNDHDDTNRILTYMGKREGENASVHLADKDRYTEEREVSYLRYTGTIPDPNDK"

sig_peptide 819..896
 /note="streptokinase signal peptide"
 mat_peptide 897..2138
 /product="streptokinase"

Alignment Scores:
 Pred. No.: 11.5 Length: 2568
 Score: 33.50 Matches: 10
 Percent Similarity: 41.94% Conservative: 3
 Best Local Similarity: 32.26% Mismatches: 6
 Query Match: 5.34% Indels: 12
 DB: 5 Gaps: 1

US-09-940-235-4 (1-259) x AAX80497 (1-2385)

Qy 168 GluThrTrpGlu-LysProTyrGlnGlyTrpMetMetValAspCysThr----- 183
 Db 1433 GAGACCTGGTCTGAAATCGTCATCAGGGTTTAAAGGAGTAACACTGTACAGTATATCCAC 1374

Qy 184 -----CysLeuGly 186
 Db 1373 ATCAACAGATTTCGCTGGTTTGTATTGGT 1343

RESULT 11
 AAX80497
 LOCUS AAX80497 2385 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 1 from patent US 6210667.
 ACCESSION ARI43998
 VERSION ARI43998.1 GI:15105865
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 2385)
 AUTHORS Reed, G.L.
 TITLE Bacterial fibrin-dependent plasminogen activator
 JOURNAL Patent: US 6210667-A 1 03-APR-2001;
 FEATURES Location/Qualifiers
 source 1..2385
 /organism="unknown"
 /mol_type="unassigned DNA"

Alignment Scores:
 Pred. No.: 12.8 Length: 2385
 Score: 33.00 Matches: 22
 Percent Similarity: 30.19% Conservative: 10
 Best Local Similarity: 20.75% Mismatches: 42
 Query Match: 5.26% Indels: 32
 DB: 1 Gaps: 5

US-09-940-235-4 (1-259) x ARI43998 (1-2385)

Qy 151 IleAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThrTrp 170
 Db 907 GTACGGCTGAAGTCTTACGAGGAGAGTGTGGCGAAAGATCCACGTATTCGCCGCCACCATG 966

Qy 171 GluLysProTyrGlnGly-----TrpMet 178
 Db 967 GAAAACGCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCGGCTTCTGGTAT 1026

Qy 179 MetValAspCysThrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgAsn 198
 Db 1027 GCCGTGCGTACTCGCGGTGATCAACGCCGCCGCGGTGTCAGATGTCGAT-----GAA 1080

Qy 199 ArgCysAsnAspGlnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLys 218
 Db 1081 GCCCTGAAGACGCCGACAGACTAATTCAGCTCGGTACCCGCG-----1122

Qy 219 AspAsnArgGlyAsnLeuLeuGlnCysIleCysThrGlyAsnGlyArg-----Gly 235
 Db 1123 -----CGGGATCCATC-----GAGGCTAGGATTGCTGGACCT 1155

Qy 236 GluTrpLysCysGluArg 241
 Db 1156 GAGTGGCTGCTAGACCGT 1173

RESULT 12
 AAX80497
 ID AAX80497 standard; cDNA; 2385 BP.
 XX AAX80497;
 AC AAX80497;
 XX AAX80497;
 DT 26-AUG-1999 (first entry)
 XX Streptokinase and maltose binding protein fusion protein encoding cDNA.
 DE Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
 KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;

KW nSK; rSK; bacterial; blood clot; thrombotic condition;
 KW myocardial infarction; venous thrombosis; pulmonary embolism;
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
 OS Streptococcus dysgalactiae subsp. equisimilis.
 OS Synthetic.
 PN WO9931247-A1.
 XX 24-JUN-1999.
 XX 15-DEC-1998; 98WO-US026694.
 XX 15-DEC-1997; 97US-0069497P.
 XX (HARD) HARVARD COLLEGE.
 PA
 PI Reed GL;
 DR WPI; 1999-395183/33.
 DR P-PSDB; AAY24797.
 XX N-terminally deleted streptokinase.
 PS Example; Page 45-48; 73pp; English.
 CC The present invention describes an isolated bacterial protein that
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical
 CC composition for dissolving blood clots. Also described are: (1) a
 CC modification comprising an isolated modified streptokinase, the
 CC (2) a method for dissolving a blood clot in a subject, comprising
 CC administering to the subject a fibrin-dependent streptokinase protein; a
 CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
 CC expression vector comprising (1); and (4) a host cell transformed with
 CC the expression vector of (3). The pharmaceutical composition comprising a
 CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
 CC blood clots in patients with a thrombotic condition, e.g. myocardial
 CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
 CC graft thrombosis and arterial thrombosis. The modified streptokinase can
 CC also be used in non-human mammals. Streptokinase activation of
 CC plasminogen is at least 10-fold, preferably 100-fold greater in the
 CC presence of fibrin than in the absence of fibrin. The modified
 CC streptokinase has at least one amino acid substitution that inactivates a
 CC substrate site for proteolytic cleavage. This reduces the rate of
 CC degradation of the streptokinase at least two-fold. The present sequence
 CC encodes a streptokinase and maltose binding protein fusion protein from
 CC an example of the present invention
 XX
 SQ Sequence 2385 BP; 745 A; 547 C; 549 G; 544 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 12.8 Length: 2385
 Score: 33.00 Matches: 22
 Percent Similarity: 30.19% Conservative: 10
 Best Local Similarity: 20.75% Mismatches: 42
 Query Match: 5.26% Indels: 32
 DB: 8 Gaps: 5

US-09-940-235-4 (1-259) x AAX80497 (1-2385)

QY 151 IleAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThrTrp 170
 DB 907 GTAGCCCTGAAGTCTTACGAGGAGAGTTCGCCGAAGATCCAGTATTGCCGCCACCATG 966
 QY 171 GluLysProTyrGlnGly-----TTPmet 178
 DB 967 GAAACGCCCAAGAGGTGAATCATCGCAACATCCGACAGATGTCGGCTTTCTGGTAT 1026
 QY 179 MetValAspCysThrCysLeuGlyGluGlySerGlyArgIleThrCysThrSerArgAsn 198
 DB 1027 GCGTGCCTACTCGGTGATCAACGCCCGCGGTGCTGACACTGTTCGAT-----GAA 1080

QY 199 ArgCysAsnAspGlnAspThrArgThrSerTyrArgIleGlyAspThrTrpSerLysLys 218
 DB 1081 GCCCTGAAGACGCGCAGACTAATTCGAGCTCGTGATCCCGC-----1122
 QY 219 AspAsnArgGlyAsnLeuLeuGlnCysIleCysThrGlyAsnGlyArg-----Gly 235
 DB 1123 -----CGGGGATCCATC-----GAGGTAGGATTGCTGGACCT 1155
 QY 236 GluTrpLysCysGluArg 241
 DB 1156 GAGTGGCTGTAGACCT 1173

RESULT 13
 AAX16632
 ID AAX16632 standard; DNA; 1242 BP.
 XX AAX16632;
 AC AAX16632;
 XX 17-OCT-2003 (revised)
 DT 04-MAY-1999 (first entry)
 XX
 DE Streptococcus equisimilis native streptokinase encoding DNA.
 XX Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
 KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;
 KW serine protease; fibrin; blood clot; thrombolytic;
 KW vascular thromboembolytic symptom; acute myocardial infarction;
 KW fibrinolysis; resistance; ds.
 XX Streptococcus dysgalactiae subsp. equisimilis.
 OS
 FH Key Location/Qualifiers
 PH CDS 1..1242
 FT /*tag= a
 FT /transl_except= (pos:40..42,aa:Asn)
 FT /note= "no stop codon given"
 XX US5876999-A.
 PN 02-MAR-1999.
 PD 06-DEC-1995; 95US-00568393.
 PF 06-DEC-1995; 95US-00568393.
 PR (NASC-) NAT SCI COUNCIL.
 PA
 XX Wu H;
 XX WPI; 1999-189643/16.
 DR P-PSDB; AAW94664.
 DR Mutant streptokinase polypeptide - useful as plasmin-resistant
 XX thrombolytic agent.
 PS Claim 1; Col 7-10; 17pp; English.
 XX The present invention describes a mutant streptokinase (SK) polypeptide
 CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
 CC segment of the corresponding native SK is replaced by another amino acid.
 CC The present sequence encodes native SK. SK is a secretory protein of
 CC haemolytic Streptococcus able to activate human plasminogen (HPlg) to
 CC plasmin (HPlm) which is a serine protease able to catalyse the
 CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
 CC agent in the treatment of vascular thromboembolytic symptoms such as
 CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
 CC is more resistant to degradation by human plasmin and is more effective
 CC both in acting as a fibrinolytic agent and in activating human plasminogen.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 1242 BP; 423 A; 268 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.3 Length: 1242
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 6 Gaps: 3

US-09-940-235-4 (1-259) x AAX16632 (1-1242)

Qy 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 538 AAGATATACTAAGCTATTGAAAAACACTAGCTATCGTGACACCATCATCTCAAGAA--- 594

Qy 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 595 -----TTACTAGCTCAAGCACAAGCATTTTAAACAAACACCCAGGCTATACG 645

Qy 238 LysCysGluArgHisThrSerValGlnThr 247
Db 646 ATTTATGAACGTGACTCTCAATCGTCACT 675

RESULT 14
AAX80492
ID AAX80492 standard; cDNA; 1242 BP.
XX
AC AAX80492;
XX
DT 17-OCT-2003 (revised)
DT 26-AUG-1999 (first entry)
XX
DE Streptococcus equisimilis native streptokinase encoding cDNA.
XX
KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
KW NSK; RSK; bacterial; blood clot; thrombotic condition;
KW myocardial infarction; venous thrombosis; pulmonary embolism;
KW cerebral thrombosis; graft thrombosis; arterial thrombosis; ss.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.

PN WO931247-A1.
XX
PD 24-JUN-1999.
XX
PF 15-DEC-1998; 98WO-US026694.
XX
PR 15-DEC-1997; 97US-0069497P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Reed GL;
XX
DR WPI; 1999-395183/33.
DR P-PSDB; AAY24794.
XX
PT N-terminally deleted streptokinase.
XX
PS Claim 44; Page 58-60; 73pp; English.

XX The present invention describes an isolated bacterial protein that
XX induces fibrin-dependent plasminogen activation in a pharmaceutical
XX composition for dissolving blood clots. Also described are: (1) a
XX composition comprising an isolated modified streptokinase, the
XX modification being removal of amino acid residues in the amino terminus;
XX (2) a method for dissolving a blood clot in a subject, comprising
XX administering to the subject a fibrin-dependent streptokinase protein; a
XX nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
XX expression vector comprising (1); and (4) a host cell transformed with
XX the expression vector of (3). The pharmaceutical composition comprising a
XX bacterial fibrin-dependent plasminogen activator is useful for dissolving
XX blood clots in patients with a thrombotic condition, e.g. myocardial
XX infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
XX graft thrombosis and arterial thrombosis. The modified streptokinase can
XX also be used in non-human mammals. Streptokinase activation of

CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC encodes native streptokinase (nsk). (Updated on 17-OCT-2003 to
CC standardise OS field)

XX SQ Sequence 1242 BP; 424 A; 267 C; 237 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.3 Length: 1242
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 7 Gaps: 3

US-09-940-235-4 (1-259) x AAX80492 (1-1242)

Qy 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 538 AAGATATACTAAGCTATTGAAAAACACTAGCTATCGTGACACCATCATCTCAAGAA--- 594

Qy 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 595 -----TTACTAGCTCAAGCACAAGCATTTTAAACAAACACCCAGGCTATACG 645

Qy 238 LysCysGluArgHisThrSerValGlnThr 247
Db 646 ATTTATGAACGTGACTCTCAATCGTCACT 675

RESULT 15
us-09-211-542a-5
Alignment Scores:
Pred. No.: 8.3 Length: 1242
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 9 Gaps: 3

US-09-940-235-4 (1-259) x us-09-211-542a-5 (1-1242)

Qy 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 538 AAGATATACTAAGCTATTGAAAAACACTAGCTATCGTGACACCATCATCTCAAGAA--- 594

Qy 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 595 -----TTACTAGCTCAAGCACAAGCATTTTAAACAAACACCCAGGCTATACG 645

Qy 238 LysCysGluArgHisThrSerValGlnThr 247
Db 646 ATTTATGAACGTGACTCTCAATCGTCACT 675

RESULT 16
us-08-568-393b-1
Alignment Scores:
Pred. No.: 8.3 Length: 1242
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 10 Gaps: 3

US-09-940-235-4 (1-259) x us-08-568-393b-1 (1-1242)

Qy 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 538 AAGATATACTAAGCTATTGAAAAACACTAGCTATCGTGACACCATCATCTCAAGAA--- 594

```

QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 595 -----TTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCAACCCAGGCTATACG 645
QY 238 LysCysGluArgHisThrSerValGlnThr 247
Db 646 ATTTATGAACGTCGACTCTCTCAATCGTCACT 675

RESULT 17
E03308
LOCUS E03308 1262 bp DNA linear PAT 29-SEP-1997
DEFINITION DNA encoding recombinant streptokinase.
ACCESSION E03308
VERSION E03308.1 GI:2171525
KEYWORDS JP 1992011892-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1262)
AUTHORS Fujii,S., Katano,T., Majima,E., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.
TITLE PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION
JOURNAL Patent: JP 1992011892-A 1 16-JAN-1992; OTSUKA PHARMACEUT FACTORY INC
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1992011892-A/1
PD 16-JAN-1992
PF 06-JUL-1990 JP 1990179851
PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR 11-APR-1990 JP 90P 96830
PI FUJII SEISUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI ONO KENJI,
PI SAKATA YASUYO, UENOYAMA TSUTOMU
PC C12N15/58, C12N1/21, C12N9/70, (C12N1/21, C12R1:19), (C12N9/70, PC C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=pSKX;
PH Key Location/Qualifiers
FH 5'UTR 1..11
FT CDS 12..1256
FT mat_peptide 12..1253
FT 3'UTR 1257..1263.
FEATURES
source Location/Qualifiers
1..1262
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Alignment Scores:
Pred. No.: 8.58 Length: 1262
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 2 Gaps: 3

US-09-940-235-4 (1-259) x E03308 (1-1262)

QY 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 552 AAAGACACATAAAGTCTGTAACAAACCTCGGTGACACCATCATCTCTCAGGAG--- 608
QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237

RESULT 19
E03308
LOCUS E03308 2568 bp DNA linear BCT 26-APR-1993
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION STREK02986
VERSION K02986.1 GI:153808
KEYWORDS streptokinase.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2568)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
COMMENT Original source text: S.equisimilis (strain H46A) DNA, clone pmf5. Draft entry and hard copy of sequence for [1] kindly provided by J.J.Ferretti, 03-SEP-1985.
The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators.

```

```

Db 609 -----CTCTGGCTCAGGCACAGTCTATCTTGAAACAAACCATCGGGCTACACT 659
QY 238 LysCysGluArgHisThrSerValGlnThr 247
Db 660 ATCTACGAACGCGACTCTTCCATCGTAACC 689

RESULT 18
E05204
LOCUS E05204 1401 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent EP 0248227.
ACCESSION I05204
VERSION I05204.1 GI:591209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Hagenson,M.J. and Stroman,D.W.
TITLE Yeast production of streptokinase
JOURNAL Patent: EP 0248227-A1 5 09-DEC-1987;
FEATURES Location/Qualifiers
source 1..1401
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 10.5 Length: 1401
Score: 31.50 Matches: 16
Percent Similarity: 48.00% Conservative: 8
Best Local Similarity: 32.00% Mismatches: 17
Query Match: 5.02% Indels: 9
DB: 3 Gaps: 3

US-09-940-235-4 (1-259) x I05204 (1-1401)

QY 203 GlnAspThrArg-----ThrSerTyrArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 547 AAAGATACTAAAGTATTGAAAACACACTAGCTATCGGTGACACCATCATCTCAAGAA--- 603
QY 221 ArgGlyAsnLeuLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 604 -----TTACTAGCTCAAGCACAAAGCATTTTAAACAAAACCAACCCAGGCTATACG 654
QY 238 LysCysGluArgHisThrSerValGlnThr 247
Db 655 ATTTATGAACGTCGACTCTCTCAATCGTCACT 684

RESULT 19
E05204
LOCUS E05204 2568 bp DNA linear BCT 26-APR-1993
DEFINITION Streptococcus equisimilis (H46A) streptokinase gene, complete cds.
ACCESSION STREK02986
VERSION K02986.1 GI:153808
KEYWORDS streptokinase.
SOURCE Streptococcus dysgalactiae subsp. equisimilis
ORGANISM Streptococcus dysgalactiae subsp. equisimilis
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2568)
AUTHORS Malke,H., Roe,B. and Ferretti,J.J.
TITLE Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H46A
JOURNAL Gene 34 (2-3), 357-362 (1985)
MEDLINE 85232082
PUBMED 2989113
COMMENT Original source text: S.equisimilis (strain H46A) DNA, clone pmf5. Draft entry and hard copy of sequence for [1] kindly provided by J.J.Ferretti, 03-SEP-1985.
The -35 and -10 regions are located at positions 760-765 and 781-786 respectively and an SD sequence at 808-813. Downstream from the coding region inverted repeats (positions 2176-2190 and 2203-2217) are thought to function as transcription terminators.

```

The nucleotide sequence of skc does not support the hypothesis that the gene has evolved by duplication and fusion, as suggested by internal two-fold AA homologies of its product.

```
FEATURES
    source
        1..2568
            /organism="Streptococcus dysgalactiae subsp. equisimilis"
            /mol_type="genomic DNA"
            /db_xref="taxon:119602"
            794..>2141
            /product="skc mRNA"
            819..2141
            /note="prestreptokinase"
            /codon_start=1
            /transl_table=11
            /protein_id="AAA26974.1"
            /db_xref="GI:153809"
            /translation="MKNYLSFGMFAALLFALTFTGVNSVQAIAGPEMLDRPSVNNNSOL
            VVSVAGTVSGTNQDISLKFEIDLTSPAHGGTEQGLSPKSPFATDSAMSHKLEK
            ALLKAIQSLIANVNSNDYFEVIDFASDATITDRNGKVFADKQSGSVLTPTQVQE
            ELLSGHVRVPYKKEPIQNOAKSDVEYTVQFTPLNPDDEFRLKDTKLLKTLAIGD
            TITSQELLAQASILNKNHPGYTYERDSSIVTHNDIFRILPMDQEFYRVKNREQ
            AYVINKSGLINEINNTDLISEKYVYLKKEKPYDPDFRSHLKLFTIKYVDVDTNELL
            KSEQLLTASERNLDFRLDYPDRDKAKLYNNLDAGFIMDYTLTGKVEDNHDNDNRIT
            VYMGKRPENASVHLAYDKDRTYTEREVYSLRYVTGTPIPNPNDK"
    sig_peptide
        819..896
            /note="streptokinase signal peptide"
    mat_peptide
        897..2138
            /product="streptokinase"
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Alignment Scores:

Pred. No.:	19.6	Length:	2568
Score:	31.50	Matches:	16
Percent Similarity:	48.00%	Conservative:	8
Best Local Similarity:	32.00%	Mismatches:	17
Query Match:	5.02%	Indels:	9
DB:	5	Gaps:	3

US-09-940-235-4 (1-259) x STRSKC (1-2568)

```
Qy 203 GinAspThrArg-----ThrSerTyArgIleGlyAspThrTrpSerLysLysAspAsn 220
Db 1434 AAAGTACTAAGTATTGAAAACAGTAGCTATCGGTGACACCATCATCTCAAGAA--- 1490
Qy 221 ArgGlyAsnLeu-----GlnCysIleCysThrGlyAsnGlyArgGlyGluTrp 237
Db 1491 -----TTACTAGCTCAAGCACAAAGCATTTTAACAAAACCCAGGCTATACG 1541
Qy 238 LysCysGluArgHisThrSerValGlnThr 247
Db 1542 ATTTATGAACGTGACTCCTCAATCGTCACT 1571
```

RESULT 20

E03308/c

LOCUS

DEFINITION DNA encoding recombinant streptokinase.

ACCESSION E03308

VERSION E03308.1 GI:2171525

KEYWORDS JP 1992011892-A/1.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 1262)

AUTHORS Fujii,S., Katano,T., Majima,B., Ogino,K., Ono,K., Sakata,Y. and Uenoyama,T.

TITLE PROTEIN OF STREPTOKINASES, CORRESPONDING GENE, CORRESPONDING PLASMID RECOMBINANT, CORRESPONDING CHARACTER TRANSFORMANT AND PRODUCTION

JOURNAL Patent: JP 1992011892-A 1 16-JAN-1992;

COMMENT OTSUKA PHARMACEUTICAL INC

OS Artificial gene

OC Artificial sequence; Genes.

PN JP 1992011892-A/1

PD 16-JAN-1992

```
PF 06-JUL-1990 JP 1990179851
PR 11-JUL-1989 JP 89P 179432, 27-NOV-1989 JP 89P 307957, PR
11-APR-1990 JP 90P 96830
PI FUJII SETSUO, KATANO TAMITAKA, MAJIMA EIJI, OGINO KOICHI, PI
ONO KENJI,
PI SAKATA YASUO, UENOYAMA TSUTOMU
PC C12N15/58,C12N1/21,C12N9/70, (C12N1/21,C12R1:19), (C12N9/70, PC
C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: clone=PSKX;
FH Key Location/Qualifiers
FT 5'UTR 1..11
FT CDS 12..1256
FT /product='recombinant streptokinase' FT
mat_peptide 12..1253
FT /product='recombinant streptokinase' FT
3'UTR 1257..1263.
FEATURES
    source
        1..1262
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Alignment Scores:
Pred. No.: 20 Length: 1262
Score: 27.00 Matches: 13
Percent Similarity: 44.44% Conservative: 3
Best Local Similarity: 36.11% Mismatches: 16
Query Match: 4.31% Indels: 4
DB: 2 Gaps: 2
US-09-940-235-4 (1-259) x E03308 (1-1262)
Qy 221 ArgGlyAsnLeuLeuGlnCysIleCysThr---GlyAsnGlyArgGlyGlu----- 236
Db 188 CGGGACAGGCCCTGTTCCGGTTTACCACCATGGCCGCGGACGAGGTGAGTTC 129
Qy 237 TrpLysCysGluArgHisThrSerValGlnThrThrSerSerGlySer 252
Db 128 GAAAAATTTCAGAGAGATGCTCGTGTAGTACCTTCAACAGTGCAGC 81
Search completed: December 6, 2004, 15:02:22
Job time : 6 secs
```

RESULT 1
AAAY24797
ID AAAY24797 standard; protein; 795 AA.
XX

Query Match 5.3%; Score 33; DB 12; Length 795;
Best Local Similarity 20.8%; Pred. No. 0.38;
Matches 22; Conservative 10; Mismatches 42; Indels 32; Gaps 5;

QY 151 IAEKCFDHAAGTSYVVGTEWEPYQG-----WMVDTCTLGEGSGRITCTSRN 198
DB 303 VALKSYEEELAKDPRIATATWENAKGEIMPNIQMSAFWYAVRTAVINAAASGRQTVD--E 360

QY 199 RCNDQDTRSYRIGDTWSKKNRGNLLQCICGTNGR---GEWKER 241
DB 361 ALKDAQTNSSVPG-----RGS1-----EGRIAGPEWLLDR 391

RESULT 3
ID AAR10194 standard; protein; 414 AA.
XX AAR10194;
XX 28-MAR-1991 (first entry)
XX Streptokinase encoded by synthetic gene.
DE Streptokinase; thrombolytic agent; myocardial infarction.
XX Synthetic.
XX EP407942-A.
XX 16-JAN-1991.
XX 11-JUL-1989; 89JP-00179432.
XX 11-JUL-1989; 89JP-00179432.
PR 27-NOV-1989; 89JP-00307957.
PR 11-APR-1990; 90JP-00096830.
XX (SAKA) OTSUKA PHARM FACTOR.
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX WPI; 1991-016179/03.
DR N-PSDB; AAQ10230.
XX Synthetic gene encoding streptokinase - scale, high purity prodn. of
PT streptokinase used as a thrombolytic agent.
XX Claim 1; Page 51; 76pp; English.
XX Streptokinase and its derivatives can be produced in large quantities
CC with high purity for use as thrombolytic agents in patients with lung
CC thrombus or myocardial infarction. See also AAR10195-R10200
XX Sequence 414 AA;

Query Match 5.0%; Score 31.5; DB 1; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGDTWSKKNRGNLL---QCICGTNGRGEWKCRHTSVQT 247
DB 180 KDTKLKTLTAIGDTITSQE---LLAQASILNKNHPGTYIERDSSIVT 225

RESULT 4
ID AAR63120 standard; protein; 414 AA.
XX AAR63120;
XX 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)

DT 16-NOV-1994 (first entry)
XX Streptokinase.
XX Streptokinase; SK; Streptococcus equisimilis; plasminogen;
XX myocardial infarction.
XX Streptococcus dysgalactiae subsp. equisimilis.
XX Key Location/Qualifiers
XX Region 1..352
FT /note= "claim 3, see CC"
FT Region 14..414
FT /note= "claim 1, see CC"
FT Region 120..352
FT /note= "claim 3, see CC"
FT Region 244..414
FT /note= "claim 3, see CC"
FT Region 244..352
FT /note= "claim 2, see CC"
XX WO9407992-A1.
XX 14-APR-1994.
XX 05-OCT-1993; 93WO-US009502.
XX 05-OCT-1992; 92US-00956692.
PR 29-SEP-1993; 93US-00128299.
XX (GEHO) GEN HOSPITAL CORP.
XX (HARD) HARVARD COLLEGE.
XX Reed GL;
XX WPI; 1994-135561/16.
XX DNA encoding a polypeptide which binds to plasminogen and corresponds to
XX region of streptokinase - useful to detect plasminogen in a sample and to
XX treat myocardial infarction.
XX Disclosure; Page 40-41; 62pp; English.
XX Nucleic acid comprising a sequence encoding amino acids 14-414 of
XX streptokinase, which binds to plasminogen and does not have a sequence
XX comprising amino acids 60-414 is new. The polypeptide pref. comprises
XX amino acids 244-352, 1-352, 120-352 or 244-414. (Updated on 25-MAR-2003
XX to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX Sequence 414 AA;

Query Match 5.0%; Score 31.5; DB 2; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGDTWSKKNRGNLL---QCICGTNGRGEWKCRHTSVQT 247
DB 180 KDTKLKTLTAIGDTITSQE---LLAQASILNKNHPGTYIERDSSIVT 225

RESULT 5
ID AAW94664 standard; protein; 414 AA.
XX AAW94664;
XX 17-OCT-2003 (revised)
DT 04-MAY-1999 (first entry)
XX Streptococcus equisimilis native streptokinase.
XX Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;
XX plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen; plasmin;

KW serine protease; fibrin; blood clot; thrombolytic;
 KW vascular thromboembolytic symptom; acute myocardial infarction;
 XX fibrinolysis; resistance.

OS Streptococcus dysgalactiae subsp. equisimilis.

PH Key Location/Qualifiers

FT Misc-difference 14 /note= "encoded by ACC"

XX US5876999-A.

XX 02-MAR-1999.

XX 06-DEC-1995; 95US-00568393.

XX 06-DEC-1995; 95US-00568393.

XX (NASC-) NAT SCI COUNCIL.

XX Wu H;

XX WPI; 1999-189643/16.

XX N-PSDB; AAX16632.

XX Mutant streptokinase polypeptide - useful as plasmin-resistant
 PT thrombolytic agent.

XX Claim 1; Col 7-10; 17pp; English.

XX The present invention describes a mutant streptokinase (SK) polypeptide
 CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61
 CC segment of the corresponding native SK is replaced by another amino acid.
 CC The present sequence represents native SK. SK is a secretory protein of
 CC haemolytic Streptococcus able to activate human plasminogen (HP1g) to
 CC plasmin (HP1m), which is a serine protease able to catalyse the
 CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic
 CC agent in the treatment of vascular thromboembolytic symptoms such as
 CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant
 CC is more resistant to degradation by human plasmin and is more effective
 CC both in acting as a fibrinolytic agent and in activating human plasminogen.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 414 AA;

Query Match 5.0%; Score 31.5; DB 3; Length 414;
 Best Local Similarity 32.0%; Pred. No. 7.6;
 Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGDTWSKDNRGMLL---QCICGTNGRGWKCRHTSVQT 247

DB 180 KDTLKLLTAIGDTITSQE-----LLAQASILNKNHPGYTIYERDSIVT 225

RESULT 6

RAY01556

ID AAY01556 standard; peptide; 414 AA.

AC AAY01556;

DT 17-OCT-2003 (revised)

DT 18-JUN-1999 (first entry)

DE Native streptokinase protein sequence.

KW Antigenic peptide; streptokinase; streptokinase-specific antibody;
 KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
 KW rheumatic fever.

OS Streptococcus dysgalactiae subsp. equisimilis.

XX WO9908698-A1.

PD 25-FEB-1999.

XX 18-AUG-1998; 98WO-US017114.

XX 18-AUG-1997; 97US-0055911P.

XX (HARD) HARVARD COLLEGE.

PA (GEO) GEN HOSPITAL CORP.

XX Reed GL, Parhami-Seren B;

XX WPI; 1999-190113/16.

XX New polypeptides which bind streptokinase-specific antibodies - useful in
 PT thrombolytic therapy.

XX Disclosure; Page 12; 44pp; English.

XX The present sequence represents a native streptokinase. The specification
 CC describes a polypeptide which binds to a streptokinase-specific antibody
 CC and prevents the antibody binding to native streptokinase. The
 CC specification also describes a synthetic polypeptide (PI) comprising an
 CC epitope which binds to an streptokinase-specific antibody and reduces
 CC thrombolytic activity of streptokinase. PI is used in thrombolytic
 CC therapy, and to prevent or treat glomerulonephritis and rheumatic fever.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 414 AA;

Query Match 5.0%; Score 31.5; DB 4; Length 414;
 Best Local Similarity 32.0%; Pred. No. 7.6;
 Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGDTWSKDNRGMLL---QCICGTNGRGWKCRHTSVQT 247

DB 180 KDTLKLLTAIGDTITSQE-----LLAQASILNKNHPGYTIYERDSIVT 225

RESULT 7

RAY24794

ID AAY24794 standard; protein; 414 AA.

XX AAY24794;

XX 17-OCT-2003 (revised)

DT 26-AUG-1999 (first entry)

DE Streptococcus equisimilis native streptokinase.

KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
 KW nSK; rSK; bacterial; blood clot; thrombotic condition;
 KW myocardial infarction; venous thrombosis; pulmonary embolism;
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis.

OS Streptococcus dysgalactiae subsp. equisimilis.

XX WO991247-A1.

XX 24-JUN-1999.

XX 15-DEC-1998; 98WO-US026694.

XX 15-DEC-1997; 97US-0069497P.

XX (HARD) HARVARD COLLEGE.

XX Reed GL;

XX WPI; 1999-395183/33.

XX N-PSDB; AAX80492.

XX N-terminally deleted streptokinase.

```
PS Claim 30; Page 60-61; 73pp; English.
XX The present invention describes an isolated bacterial protein that
CC induces fibrin-dependent plasminogen activation in a pharmaceutical
CC composition for dissolving blood clots. Also described are: (1) a
CC composition comprising an isolated modified streptokinase, the
CC modification being removal of amino acid residues in the amino terminus;
CC (2) a method for dissolving a blood clot in a subject, comprising
CC administering to the subject a fibrin-dependent streptokinase protein; a
CC nucleic acid (1) encoding a modified bacterial streptokinase; (3) an
CC expression vector comprising (1); and (4) a host cell transformed with
CC the expression vector of (3). The pharmaceutical composition comprising a
CC bacterial fibrin-dependent plasminogen activator is useful for dissolving
CC blood clots in patients with a thrombotic condition, e.g. myocardial
CC infarction, venous thrombosis, pulmonary embolism, cerebral thrombosis,
CC graft thrombosis and arterial thrombosis. The modified streptokinase can
CC also be used in non-human mammals. Streptokinase activation of
CC plasminogen is at least 10-fold, preferably 100-fold greater in the
CC presence of fibrin than in the absence of fibrin. The modified
CC streptokinase has at least one amino acid substitution that inactivates a
CC substrate site for proteolytic cleavage. This reduces the rate of
CC degradation of the streptokinase at least two-fold. The present sequence
CC represents native streptokinase (nsk). (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 414 AA;

Query Match          5.0%; Score 31.5; DB 5; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRGNLL---QCICGTNGRGWKCRRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 8
pct-us93-09502-1

Query Match          5.0%; Score 31.5; DB 7; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRGNLL---QCICGTNGRGWKCRRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 9
us-08-128-299-1

Query Match          5.0%; Score 31.5; DB 8; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRGNLL---QCICGTNGRGWKCRRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 10
us-09-211-542a-6

Query Match          5.0%; Score 31.5; DB 10; Length 414;
Best Local Similarity 32.0%; Pred. No. 7.6;
Matches 16; Conservative 8; Mismatches 17; Indels 9; Gaps 3;

QY 203 QDTR--TSYRIGTWSKNGRGNLL---QCICGTNGRGWKCRRHTSVQT 247
Db 180 KTKLKLTLAIGDTITSQE---LLAQASILNKNHPGYTIYERDSSIVT 225

RESULT 11
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STRP_STRSQ
ID STRP_STRSQ STANDARD; PRT; 440 AA.
AC P00779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Streptokinase C precursor.
GN Name=sk;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=H46A;
RX MEDLINE=85232082; PubMed=2989113;
RA Malke H., Roe B., Ferretti J.J.;
RT "Nucleotide sequence of the streptokinase gene from Streptococcus
RT equisimilis H46A."
RL Gene 34:357-362(1985).
RN [2]
RP SEQUENCE OF 27-440.
RX MEDLINE=83127125; PubMed=6760891;
RA Jackson K.W., Tang J.;
RT "Complete amino acid sequence of streptokinase and its homology with
RT serine proteases."
RL Biochemistry 21:6620-6625(1982).
CC -1- FUNCTION: This protein is not a protease, but it activates
CC plasminogen by complexing with it. As a potential virulence
CC factor, it is thought to prevent the formation of effective fibrin
CC barriers around the site of infection, thereby contributing to the
CC invasiveness of the cells.
CC -----
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CC -----
CC EMBL; K02986; AAA26974.1; -.
CC EMBL; X72832; CAA51351.1; -.
CC PIR; A00967; BZSO.
CC PIR; A22801; A22801.
CC PDB; 1L4D; X-ray; B=40-173.
CC PDB; 1L4Z; X-ray; B=26-173.
CC InterPro; IPR004093; Staphylokinase.
CC InterPro; IPR008124; Streptokinase.
CC Pfam; PF02821; Staphylokinase; 3.
CC PRINTS; PR01753; STREPKINASE.
CC 3D-structure; Direct protein sequencing; Plasminogen activation;
CC Signal; Virulence.
CC SIGNAL 1 26
CC CHAIN 27 440 Streptokinase C.
CC VARIANT 195 195 L -> D.
CC VARIANT 207 207 D -> L.
CC CONFLICT 298 300 EKY -> LEYK (in Ref. 2).
CC CONFLICT 438 438 N -> D (in Ref. 2).
CC STRAND 180 180
CC STRAND 184 194
CC TURN 199 200
CC TURN 203 204
CC STRAND 205 205
CC STRAND 209 214
CC TURN 216 217
CC STRAND 219 221
CC HELIX 222 236
CC TURN 238 239
CC STRAND 240 252
CC TURN 253 254
CC STRAND 259 260
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